

[illegible]

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
0	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

[illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible]

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
0	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

[illegible]

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
0	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

[illegible][illegible][illegible]

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
0	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

[illegible][illegible][illegible][illegible][illegible][illegible]

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
0	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
0	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

att Ile	gaa Glu 75	cgc Arg	ctt Leu	ggc Gly	ata Ile	tcc Ser 80	tac Tyr	cac His	ttt Phe	gag Glu	aaa Lys 85	gaa Glu	att Ile	gat Asp	gat Asp	291
att Ile 90	ttg Leu	gat Asp	cag Gln	att Ile	tac Tyr 95	aac Asn	caa Gln	aac Asn	tca Ser	aac Asn 100	tgc Cys	aac Asn	gat Asp	ttg Leu	tgc Cys 105	339
act Thr	tct Ser	gca Ala	ctt Leu	caa Gln 110	ttt Phe	cga Arg	ttg Leu	ctc Leu	agg Arg 115	caa Gln	cat His	ggt Gly	ttc Phe	aac Asn 120	atc Ile	387
tct Ser	cct Pro	gaa Glu	att Ile 125	ttc Phe	agc Ser	aaa Lys	ttc Phe	caa Gln 130	gac Asp	gaa Glu	aat Asn	ggc Gly 135	aaa Lys 135	ttc Phe	aag Lys	435
gaa Glu	tct Ser	ctt Leu 140	gct Ala	agt Ser	gat Asp	gtc Val 145	tta Leu	gga Gly	tta Leu	ttg Leu	aac Asn 150	ttg Leu	tat Tyr	gaa Glu	gct Ala	483
tca Ser	cat His 155	gta Val	agg Arg	act Thr	cat His	gct Ala 160	gac Asp	gat Asp	atc Ile	tta Leu 165	gaa Glu 165	gac Asp	gca Ala	ctt Leu	gct Ala	531
ttc Phe 170	tcc Ser	act Thr	atc Ile	cat His	ctt Leu 175	gaa Glu	tct Ser	gca Ala	gct Ala	cca Pro 180	cat His	ttg Leu 180	aaa Lys	tct Ser	cca Pro 185	579
ctt Leu	agg Arg	gag Glu	caa Gln 190	gtg Val	aca Thr	cat His	gcc Ala	ctt Leu	gag Glu 195	caa Gln 195	tgt Cys	ttg Leu	cac His 200	aag Lys	ggc Gly	627
gtt Val	cct Pro	aga Arg 205	gtc Val	gag Glu	acc Thr	cga Arg	ttc Phe	ttc Phe 210	atc Ile	tca Ser	tca Ser	atc Ile 215	tat Tyr	gac Asp	aag Lys	675
gaa Glu	caa Gln 220	tcg Ser	aag Lys	aat Asn	aat Asn	gtg Val 225	tta Leu	ctt Leu	cga Arg	ttt Phe	gcc Ala 230	aaa Lys 230	ttg Leu	gat Asp	ttc Phe	723
aac Asn 235	ttg Leu	ctc Leu	cag Gln	atg Met	ttg Leu	cac His 240	aaa Lys	caa Gln	gaa Glu	ctt Leu 245	gct Ala	caa Gln	gta Val	tca Ser	agg Arg	771
tgg Trp 250	tgg Trp	aaa Lys	gat Asp	ttg Leu	gat Asp 255	ttt Phe	gta Val	aca Thr	aca Thr	ctt Leu 260	cca Pro	tat Tyr	gct Ala	aga Arg	gat Asp 265	819
cga Arg	gta Val	gtt Val	gaa Glu	tgc Cys 270	tac Tyr	ttt Phe	tgg Trp	gca Ala	tta Leu 275	gga Gly	gtt Val	tat Tyr	ttt Phe	gag Glu 280	cct Pro	867
caa Gln	tac Tyr	tct Ser	caa Gln 285	gct Ala	cgc Arg	gtc Val	atg Met	ctc Leu 290	gtt Val	aag Lys	acc Thr	ata Ile 295	tca Ser	atg Met	att Ile	915

tcg Ser	att Ile	gtc Val 300	gat Asp	gac Asp	acc Thr	ttt Phe	gat Asp 305	gct Ala	tac Tyr	ggt Gly	aca Thr	gtt Val 310	aaa Lys	gaa Glu	ctt Leu	963
gag Glu	gca Ala 315	tac Tyr	aca Thr	gat Asp	gcc Ala	ata Ile 320	caa Gln	aga Arg	tgg Trp	gat Asp	atc Ile 325	aac Asn	gaa Glu	att Ile	gat Asp	1011
cgg Arg 330	ctt Leu	cct Pro	gat Asp	tac Tyr	atg Met 335	aaa Lys	atc Ile	agt Ser	tac Tyr	aaa Lys 340	gct Ala	att Ile	cta Leu	gat Asp	ctc Leu 345	1059
tac Tyr	aag Lys	gat Asp	tat Tyr	gaa Glu 350	aag Lys	gaa Glu	ttg Leu	tct Ser	agt Ser 355	gcc Ala	gga Gly	aga Arg	tct Ser	cat His 360	att Ile	1107
gtc Val	tgc Cys	cat His 365	gca Ala	ata Ile	gaa Glu	aga Arg	atg Met 370	aaa Lys	gaa Glu	gta Val	gta Val	aga Arg	aat Asn 375	tat Tyr	aat Asn	1155
gtc Val	gag Glu 380	tca Ser	aca Thr	tgg Trp	ttt Phe	att Ile	gaa Glu 385	gga Gly	tat Tyr	acg Thr	cca Pro	cct Pro 390	gtt Val	tct Ser	gaa Glu	1203
tac Tyr	cta Leu 395	agc Ser	aat Asn	gca Ala	cta Leu	gca Ala	act Thr 400	acc Thr	aca Thr	tat Tyr	tac Tyr 405	tac Tyr	ctc Leu	gcg Ala	aca Thr	1251
aca Thr 410	tcg Ser	tat Tyr	ttg Leu	ggc Gly	atg Met 415	aag Lys	tct Ser	gcc Ala	acg Thr	gag Glu 420	caa Gln	gat Asp	ttt Phe	gag Glu	tgg Trp 425	1299
ttg Leu	tca Ser	aag Lys	aat Asn	cca Pro 430	aaa Lys	att Ile	ctt Leu	gaa Glu	gct Ala 435	agt Ser	gta Val	att Ile	ata Ile	tgt Cys 440	cga Arg	1347
gtt Val	atc Ile	gat Asp 445	gac Asp	aca Thr	gcc Ala	acg Thr	tac Tyr	gag Glu 450	gtt Val	gag Glu	aaa Lys	agc Ser	agg Arg	gga Gly	caa Gln	1395
att Ile	gca Ala 460	act Thr	gga Gly	att Ile	gag Glu	tgc Cys	tgc Cys	atg Met	aga Arg	gat Asp	tat Tyr 470	ggt Gly	ata Ile	tca Ser	aca Thr	1443
aaa Lys	gag Glu 475	gca Ala	atg Met	gct Ala	aaa Lys	ttt Phe 480	caa Gln	aat Asn	atg Met	gct Ala	gag Glu 485	aca Thr	gca Ala	tgg Trp	aaa Lys	1491
gat Asp 490	att Ile	aat Asn	gaa Glu	gga Gly	ctt Leu 495	ctt Leu	agg Arg	ccc Pro	act Thr	ccc Pro 500	gtc Val	tct Ser	aca Thr	gaa Glu	ttt Phe 505	1539
tta Leu	act Thr	cct Pro	att Ile	ctc Leu 510	aat Asn	ctt Leu	gct Ala	cgt Arg	att Ile 515	gtt Val	gag Glu	gtt Val	aca Thr	tat Tyr 520	ata Ile	1587
cac	aat	cta	gat	gga	tac	act	cat	ccg	gag	aaa	gtc	tta	aaa	cct	cac	1635

<400>	2														
Met	Ala	Ser	Ala	Ala	Val	Ala	Asn	Tyr	Glu	Glu	Glu	Ile	Val	Arg	Pro
1				5					10					15	
Val	Ala	Asp	Phe	Ser	Pro	Ser	Leu	Trp	Gly	Asp	Gln	Phe	Leu	Ser	Phe
			20					25					30		
Ser	Ile	Lys	Asn	Gln	Val	Ala	Glu	Lys	Tyr	Ala	Gln	Glu	Ile	Glu	Ala
		35					40					45			
Leu	Lys	Glu	Gln	Thr	Arg	Asn	Met	Leu	Leu	Ala	Thr	Gly	Met	Lys	Leu
	50					55					60				
Ala	Asp	Thr	Leu	Asn	Leu	Ile	Asp	Thr	Ile	Glu	Arg	Leu	Gly	Ile	Ser
65					70					75					80
Tyr	His	Phe	Glu	Lys	Glu	Ile	Asp	Asp	Ile	Leu	Asp	Gln	Ile	Tyr	Asn
				85					90					95	
Gln	Asn	Ser	Asn	Cys	Asn	Asp	Leu	Cys	Thr	Ser	Ala	Leu	Gln	Phe	Arg
			100					105					110		
Leu	Leu	Arg	Gln	His	Gly	Phe	Asn	Ile	Ser	Pro	Glu	Ile	Phe	Ser	Lys
		115					120					125			
Phe	Gln	Asp	Glu	Asn	Gly	Lys	Phe	Lys	Glu	Ser	Leu	Ala	Ser	Asp	Val
	130					135					140				
Leu	Gly	Leu	Leu	Asn	Leu	Tyr	Glu	Ala	Ser	His	Val	Arg	Thr	His	Ala
145					150					155					160
Asp	Asp	Ile	Leu	Glu	Asp	Ala	Leu	Ala	Phe	Ser	Thr	Ile	His	Leu	Glu
				165					170					175	
Ser	Ala	Ala	Pro	His	Leu	Lys	Ser	Pro	Leu	Arg	Glu	Gln	Val	Thr	His
			180					185					190		
Ala	Leu	Glu	Gln	Cys	Leu	His	Lys	Gly	Val	Pro	Arg	Val	Glu	Thr	Arg
		195					200					205			
Phe	Phe	Ile	Ser	Ser	Ile	Tyr	Asp	Lys	Glu	Gln	Ser	Lys	Asn	Asn	Val
	210					215					220				
Leu	Leu	Arg	Phe	Ala	Lys	Leu	Asp	Phe	Asn	Leu	Leu	Gln	Met	Leu	His
225					230					235					240
Lys	Gln	Glu	Leu	Ala	Gln	Val	Ser	Arg	Trp	Trp	Lys	Asp	Leu	Asp	Phe
				245					250					255	
Val	Thr	Thr	Leu	Pro	Tyr	Ala	Arg	Asp	Arg	Val	Val	Glu	Cys	Tyr	Phe
			260					265					270		
Trp	Ala	Leu	Gly	Val	Tyr	Phe	Glu	Pro	Gln	Tyr	Ser	Gln	Ala	Arg	Val
		275					280					285			
Met	Leu	Val	Lys	Thr	Ile	Ser	Met	Ile	Ser	Ile	Val	Asp	Asp	Thr	Phe
	290					295					300				
Asp	Ala	Tyr	Gly	Thr	Val	Lys	Glu	Leu	Glu	Ala	Tyr	Thr	Asp	Ala	Ile
				310						315					320
Gln	Arg	Trp	Asp	Ile	Asn	Glu	Ile	Asp	Arg	Leu	Pro	Asp	Tyr	Met	Lys
				325					330					335	
Ile	Ser	Tyr	Lys	Ala	Ile	Leu	Asp	Leu	Tyr	Lys	Asp	Tyr	Glu	Lys	Glu

340 345 350  
 Leu Ser Ser Ala Gly Arg Ser His Ile Val Cys His Ala Ile Glu Arg  
 355 360 365  
 Met Lys Glu Val Val Arg Asn Tyr Asn Val Glu Ser Thr Trp Phe Ile  
 370 375 380  
 Glu Gly Tyr Thr Pro Pro Val Ser Glu Tyr Leu Ser Asn Ala Leu Ala  
 385 390 395 400  
 Thr Thr Thr Tyr Tyr Tyr Leu Ala Thr Thr Ser Tyr Leu Gly Met Lys  
 405 410 415  
 Ser Ala Thr Glu Gln Asp Phe Glu Trp Leu Ser Lys Asn Pro Lys Ile  
 420 425 430  
 Leu Glu Ala Ser Val Ile Ile Cys Arg Val Ile Asp Asp Thr Ala Thr  
 435 440 445  
 Tyr Glu Val Glu Lys Ser Arg Gly Gln Ile Ala Thr Gly Ile Glu Cys  
 450 455 460  
 Cys Met Arg Asp Tyr Gly Ile Ser Thr Lys Glu Ala Met Ala Lys Phe  
 465 470 475 480  
 Gln Asn Met Ala Glu Thr Ala Trp Lys Asp Ile Asn Glu Gly Leu Leu  
 485 490 495  
 Arg Pro Thr Pro Val Ser Thr Glu Phe Leu Thr Pro Ile Leu Asn Leu  
 500 505 510  
 Ala Arg Ile Val Glu Val Thr Tyr Ile His Asn Leu Asp Gly Tyr Thr  
 515 520 525  
 His Pro Glu Lys Val Leu Lys Pro His Ile Ile Asn Leu Leu Val Asp  
 530 535 540  
 Ser Ile Lys Ile  
 545

<210> 3

<211> 1644

<212> DNA

<213> Nicotiana tabacum

<220>

<221> CDS

<222> (1)...(1644)

<400> 3

atg gcc tca gca gca gtt gca aac tat gaa gaa gag att gtt cgc ccc 48  
 Met Ala Ser Ala Ala Val Ala Asn Tyr Glu Glu Glu Ile Val Arg Pro  
 1 5 10 15

gtc gcc gac ttc tcc cct agt ctc tgg ggt gat cag ttc ctt tca ttc 96  
 Val Ala Asp Phe Ser Pro Ser Leu Trp Gly Asp Gln Phe Leu Ser Phe  
 20 25 30

tcc att gat aat cag gtt gcg gaa aag tat gct caa gag att gaa gca 144  
 Ser Ile Asp Asn Gln Val Ala Glu Lys Tyr Ala Gln Glu Ile Glu Ala  
 35 40 45

ttg aag gaa caa acg agg agt atg ctg tta gca acc gga agg aaa ttg 192  
 Leu Lys Glu Gln Thr Arg Ser Met Leu Leu Ala Thr Gly Arg Lys Leu  
 50 55 60

gcc gat aca ttg aat ttg att gac att att gaa cgc ctt ggt ata tcc 240  
 Ala Asp Thr Leu Asn Leu Ile Asp Ile Ile Glu Arg Leu Gly Ile Ser  
 65 70 75 80

T.08330"02330660

[illegible]

gat gct tac ggt aca gtt aaa gaa ctt gag gca tac aca gat gcc ata	960
Asp Ala Tyr Gly Thr Val Lys Glu Leu Glu Ala Tyr Thr Asp Ala Ile	
305 310 315 320	
caa aga tgg gat atc aac gaa att gat cgg ctt cct gat tac atg aaa	1008
Gln Arg Trp Asp Ile Asn Glu Ile Asp Arg Leu Pro Asp Tyr Met Lys	
325 330 335	
atc agt tat aaa gct att cta gat ctc tac aag gat tat gaa aag gaa	1056
Ile Ser Tyr Lys Ala Ile Leu Asp Leu Tyr Lys Asp Tyr Glu Lys Glu	
340 345 350	
ttg tct agt gcc gga aga tct cat att gtc tgc cat gca ata gaa aga	1104
Leu Ser Ser Ala Gly Arg Ser His Ile Val Cys His Ala Ile Glu Arg	
355 360 365	
atg aaa gaa gta gta aga aat tat aat gtc gag tca aca tgg ttt att	1152
Met Lys Glu Val Val Arg Asn Tyr Asn Val Glu Ser Thr Trp Phe Ile	
370 375 380	
gaa gga tat atg cca cct gtt tct gaa tac cta agc aat gca cta gca	1200
Glu Gly Tyr Met Pro Pro Val Ser Glu Tyr Leu Ser Asn Ala Leu Ala	
385 390 395 400	
act acc aca tat tac tac ctc gcg aca aca tcg tat ttg ggc atg aag	1248
Thr Thr Thr Tyr Tyr Tyr Leu Ala Thr Thr Ser Tyr Leu Gly Met Lys	
405 410 415	
tct gcc acg gag caa gat ttt gag tgg ttg tca aag aat cca aaa att	1296
Ser Ala Thr Glu Gln Asp Phe Glu Trp Leu Ser Lys Asn Pro Lys Ile	
420 425 430	
ctt gaa gct agt gta att ata tgt cga gtt atc gat gac aca gcc acg	1344
Leu Glu Ala Ser Val Ile Ile Cys Arg Val Ile Asp Asp Thr Ala Thr	
435 440 445	
tac gag gtt gag aaa agc agg gga caa att gca act gga att gag tgc	1392
Tyr Glu Val Glu Lys Ser Arg Gly Gln Ile Ala Thr Gly Ile Glu Cys	
450 455 460	
tgc atg aga gat tat ggt ata tca aca aaa gag gca atg gct aaa ttt	1440
Cys Met Arg Asp Tyr Gly Ile Ser Thr Lys Glu Ala Met Ala Lys Phe	
465 470 475 480	
caa aat atg gct gag aca gca tgg aaa gat att aat gaa gga ctt ctt	1488
Gln Asn Met Ala Glu Thr Ala Trp Lys Asp Ile Asn Glu Gly Leu Leu	
485 490 495	
agg ccc act ccc gtc tct aca gaa ttt tta act cct att ctc aat ctt	1536
Arg Pro Thr Pro Val Ser Thr Glu Phe Leu Thr Pro Ile Leu Asn Leu	
500 505 510	
gct cgt att gtt gag gtt aca tat ata cac aat cta gat gga tac act	1584
Ala Arg Ile Val Glu Val Thr Tyr Ile His Asn Leu Asp Gly Tyr Thr	
515 520 525	
cat ccg gag aaa gtc tta aaa cct cac att att aac cta ctt gtg gac	1632

tcc atc aaa att  
Ser Ile Lys Ile  
545

```
<210> 4
<211> 548
<212> PRT
<213> Nicotiana tabacum
```

	<400> 4														
Met 1	Ala	Ser	Ala	Ala 5	Val	Ala	Asn	Tyr	Glu 10	Glu	Glu	Ile	Val	Arg 15	Pro
Val	Ala	Asp	Phe 20	Ser	Pro	Ser	Leu 25	Trp	Gly	Asp	Gln	Phe 30	Leu	Ser	Phe
Ser	Ile	Asp 35	Asn	Gln	Val	Ala	Glu 40	Lys	Tyr	Ala	Gln	Glu 45	Ile	Glu	Ala
Leu	Lys 50	Glu	Gln	Thr	Arg	Ser 55	Met	Leu	Leu	Ala	Thr 60	Gly	Arg	Lys	Leu
Ala 65	Asp	Thr	Leu	Asn 70	Leu	Ile	Asp	Ile	Ile 75	Glu	Arg	Leu	Gly	Ile	Ser 80
Tyr	His	Phe	Glu 85	Lys	Glu	Ile	Asp	Glu 90	Ile	Leu	Asp	Gln 95	Ile	Tyr	Asn
Gln	Asn	Ser 100	Asn	Cys	Asn	Asp	Leu 105	Cys	Thr	Ser	Ala	Leu 110	Gln	Phe	Arg
Leu	Leu	Arg 115	Gln	His	Gly	Phe	Asn 120	Ile	Ser	Pro	Glu	Ile 125	Phe	Ser	Lys
Phe	Gln 130	Asp	Glu	Asn	Gly 135	Lys	Phe	Lys	Glu	Ser	Leu 140	Ala	Ser	Asp	Val
Leu 145	Gly	Leu	Leu	Asn 150	Leu	Tyr	Glu	Ala	Ser	His 155	Val	Arg	Thr	His	Ala 160
Asp	Asp	Ile	Leu	Glu 165	Asp	Ala	Leu	Ala 170	Phe	Ser	Thr	Ile	His	Leu	Glu 175
Ser	Ala	Ala 180	Pro	His	Leu	Lys	Ser	Pro 185	Leu	Arg	Glu	Gln	Val 190	Thr	His
Ala	Leu	Glu 195	Gln	Cys	Leu	His	Lys 200	Gly	Val	Pro	Arg	Val 205	Glu	Thr	Arg
Phe	Phe 210	Ile	Ser	Ser	Ile	Tyr 215	Asp	Lys	Glu	Gln	Ser 220	Lys	Asn	Asn	Val
Leu 225	Leu	Arg	Phe	Ala	Lys 230	Leu	Asp	Phe	Asn	Leu	Leu 235	Gln	Met	Leu	His 240
Lys	Gln	Glu	Leu	Ala 245	Gln	Val	Ser	Arg	Trp 250	Trp	Lys	Asp	Leu	Asp 255	Phe
Val	Thr	Thr	Leu 260	Pro	Tyr	Ala	Arg	Asp 265	Arg	Val	Val	Glu	Cys	Tyr	Phe
Glu	Ala	Leu 275	Gly	Val	Tyr	Phe	Glu	Pro 280	Gln	Tyr	Ser	Gln	Ala	Arg	Val
Met	Leu 290	Val	Lys	Thr	Ile	Ser 295	Met	Ile	Ser	Ile	Val 300	Asp	Asp	Thr	Phe
Asp 305	Ala	Tyr	Gly	Thr	Val	Lys 310	Glu	Leu	Glu	Ala 315	Tyr	Thr	Asp	Ala	Ile 320
Gln	Arg	Trp	Asp	Ile 325	Asn	Glu	Ile	Asp	Arg 330	Leu	Pro	Asp	Tyr	Met	Lys
Ile	Ser	Tyr	Lys	Ala	Ile	Leu	Asp	Leu	Tyr	Lys	Asp	Tyr	Glu	Lys	Glu



340 345 350  
 Leu Ser Ser Ala Gly Arg Ser His Ile Val Cys His Ala Ile Glu Arg  
 355 360 365  
 Met Lys Glu Val Val Arg Asn Tyr Asn Val Glu Ser Thr Trp Phe Ile  
 370 375 380  
 Glu Gly Tyr Met Pro Pro Val Ser Glu Tyr Leu Ser Asn Ala Leu Ala  
 385 390 395 400  
 Thr Thr Thr Tyr Tyr Tyr Leu Ala Thr Thr Ser Tyr Leu Gly Met Lys  
 405 410 415  
 Ser Ala Thr Glu Gln Asp Phe Glu Trp Leu Ser Lys Asn Pro Lys Ile  
 420 425 430  
 Leu Glu Ala Ser Val Ile Ile Cys Arg Val Ile Asp Asp Thr Ala Thr  
 435 440 445  
 Tyr Glu Val Glu Lys Ser Arg Gly Gln Ile Ala Thr Gly Ile Glu Cys  
 450 455 460  
 Cys Met Arg Asp Tyr Gly Ile Ser Thr Lys Glu Ala Met Ala Lys Phe  
 465 470 475 480  
 Gln Asn Met Ala Glu Thr Ala Trp Lys Asp Ile Asn Glu Gly Leu Leu  
 485 490 495  
 Arg Pro Thr Pro Val Ser Thr Glu Phe Leu Thr Pro Ile Leu Asn Leu  
 500 505 510  
 Ala Arg Ile Val Glu Val Thr Tyr Ile His Asn Leu Asp Gly Tyr Thr  
 515 520 525  
 His Pro Glu Lys Val Leu Lys Pro His Ile Ile Asn Leu Leu Val Asp  
 530 535 540  
 Ser Ile Lys Ile  
 545

&lt;210&gt; 5

&lt;211&gt; 1644

&lt;212&gt; DNA

&lt;213&gt; Nicotiana tabacum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1644)

&lt;400&gt; 5

atg gcc tca gca gca gtt gca aac tat gaa gaa gag att gtt cgc ccc	48
Met Ala Ser Ala Ala Val Ala Asn Tyr Glu Glu Glu Ile Val Arg Pro	
1 5 10 15	
gtc gcc gac ttc tcc cct agt ctc tgg ggt gat cag ttc ctt tca ttc	96
Val Ala Asp Phe Ser Pro Ser Leu Trp Gly Asp Gln Phe Leu Ser Phe	
20 25 30	
tcc att gat aat cag gtt gcg gaa aag tat gct caa gag att gaa gca	144
Ser Ile Asp Asn Gln Val Ala Glu Lys Tyr Ala Gln Glu Ile Glu Ala	
35 40 45	
ttg aag gaa caa acg agg agt atg ctg tta gca acc gga agg aaa ttg	192
Leu Lys Glu Gln Thr Arg Ser Met Leu Leu Ala Thr Gly Arg Lys Leu	
50 55 60	
gcc gat aca ttg aat ttg att gac att att gaa cgc ctt ggt ata tcc	240
Ala Asp Thr Leu Asn Leu Ile Asp Ile Ile Glu Arg Leu Gly Ile Ser	
65 70 75 80	

T03290"0286550

tac cac ttt gag aaa gaa att gat gag att ttg gat cag att tac aac	288
Tyr His Phe Glu Lys Glu Ile Asp Glu Ile Leu Asp Gln Ile Tyr Asn	
85 90 95	
caa aac tca aac tgc aat gat ttg tgc acc tct gca ctt caa ttt cga	336
Gln Asn Ser Asn Cys Asn Asp Leu Cys Thr Ser Ala Leu Gln Phe Arg	
100 105 110	
ttg ctc agg caa cac ggt ttc aac atc tct cct gaa att ttc agc aaa	384
Leu Leu Arg Gln His Gly Phe Asn Ile Ser Pro Glu Ile Phe Ser Lys	
115 120 125	
ttc caa gat gaa aat ggc aaa ttc aag gag tct ctt gct agt gat gtc	432
Phe Gln Asp Glu Asn Gly Lys Phe Lys Glu Ser Leu Ala Ser Asp Val	
130 135 140	
tta gga tta tta aac ttg tat gaa gct tca cat gta agg act cat gct	480
Leu Gly Leu Leu Asn Leu Tyr Glu Ala Ser His Val Arg Thr His Ala	
145 150 155 160	
gac gat atc tta gaa gac gca ctt gct ttc tcc act atc cat ctt gaa	528
Asp Asp Ile Leu Glu Asp Ala Leu Ala Phe Ser Thr Ile His Leu Glu	
165 170 175	
tct gca gct cca cat ttg aaa tct cca ctt agg gag caa gtg aca cat	576
Ser Ala Ala Pro His Leu Lys Ser Pro Leu Arg Glu Gln Val Thr His	
180 185 190	
gcc ctt gag caa tgt ttg cac aag ggt gtt cct aga gtc gag acc cga	624
Ala Leu Glu Gln Cys Leu His Lys Gly Val Pro Arg Val Glu Thr Arg	
195 200 205	
ttc ttc atc tca tca atc tat gac aag gaa caa tcg aag aat aat gtg	672
Phe Phe Ile Ser Ser Ile Tyr Asp Lys Glu Gln Ser Lys Asn Asn Val	
210 215 220	
tta ctt cga ttt gcc aaa ttg gat ttc aac ttg ctc cag atg ttg cac	720
Leu Leu Arg Phe Ala Lys Leu Asp Phe Asn Leu Leu Gln Met Leu His	
225 230 235 240	
aaa caa gaa ctt gct caa gta tca agg tgg tgg aaa gat ttg gat ttt	768
Lys Gln Glu Leu Ala Gln Val Ser Arg Trp Trp Lys Asp Leu Asp Phe	
245 250 255	
gta aca aca ctt cca tat gct aga gat cga gta gtt gaa tgc tac ttt	816
Val Thr Thr Leu Pro Tyr Ala Arg Asp Arg Val Val Glu Cys Tyr Phe	
260 265 270	
tgg gca tta gga gtt tat ttt gag cct caa tac tct caa gct cgc gtc	864
Trp Ala Leu Gly Val Tyr Phe Glu Pro Gln Tyr Ser Gln Ala Arg Val	
275 280 285	
atg ctc gtt aag acc ata tca atg att tcg att gtc gat gac acc ttt	912
Met Leu Val Lys Thr Ile Ser Met Ile Ser Ile Val Asp Asp Thr Phe	
290 295 300	



His Pro Glu Lys Val Leu Lys Pro His Ile Ile Asn Leu Leu Val Asp  
 530 535 540

tcc atc aaa att  
 Ser Ile Lys Ile  
 545

1644

&lt;210&gt; 6

&lt;211&gt; 548

&lt;212&gt; PRT

&lt;213&gt; Nicotiana tabacum

&lt;400&gt; 6

Met Ala Ser Ala Ala Val Ala Asn Tyr Glu Glu Glu Ile Val Arg Pro  
 1 5 10 15  
 Val Ala Asp Phe Ser Pro Ser Leu Trp Gly Asp Gln Phe Leu Ser Phe  
 20 25 30  
 Ser Ile Asp Asn Gln Val Ala Glu Lys Tyr Ala Gln Glu Ile Glu Ala  
 35 40 45  
 Leu Lys Glu Gln Thr Arg Ser Met Leu Leu Ala Thr Gly Arg Lys Leu  
 50 55 60  
 Ala Asp Thr Leu Asn Leu Ile Asp Ile Ile Glu Arg Leu Gly Ile Ser  
 65 70 75 80  
 Tyr His Phe Glu Lys Glu Ile Asp Glu Ile Leu Asp Gln Ile Tyr Asn  
 85 90 95  
 Gln Asn Ser Asn Cys Asn Asp Leu Cys Thr Ser Ala Leu Gln Phe Arg  
 100 105 110  
 Leu Leu Arg Gln His Gly Phe Asn Ile Ser Pro Glu Ile Phe Ser Lys  
 115 120 125  
 Phe Gln Asp Glu Asn Gly Lys Phe Lys Glu Ser Leu Ala Ser Asp Val  
 130 135 140  
 Leu Gly Leu Leu Asn Leu Tyr Glu Ala Ser His Val Arg Thr His Ala  
 145 150 155 160  
 Asp Asp Ile Leu Glu Asp Ala Leu Ala Phe Ser Thr Ile His Leu Glu  
 165 170 175  
 Ser Ala Ala Pro His Leu Lys Ser Pro Leu Arg Glu Gln Val Thr His  
 180 185 190  
 Ala Leu Glu Gln Cys Leu His Lys Gly Val Pro Arg Val Glu Thr Arg  
 195 200 205  
 Phe Phe Ile Ser Ser Ile Tyr Asp Lys Glu Gln Ser Lys Asn Asn Val  
 210 215 220  
 Leu Leu Arg Phe Ala Lys Leu Asp Phe Asn Leu Leu Gln Met Leu His  
 225 230 235 240  
 Lys Gln Glu Leu Ala Gln Val Ser Arg Trp Trp Lys Asp Leu Asp Phe  
 245 250 255  
 Val Thr Thr Leu Pro Tyr Ala Arg Asp Arg Val Val Glu Cys Tyr Phe  
 260 265 270  
 Trp Ala Leu Gly Val Tyr Phe Glu Pro Gln Tyr Ser Gln Ala Arg Val  
 275 280 285  
 Met Leu Val Lys Thr Ile Ser Met Ile Ser Ile Val Asp Asp Thr Phe  
 290 295 300  
 Asp Ala Tyr Gly Thr Val Lys Glu Leu Glu Ala Tyr Thr Asp Ala Ile  
 305 310 315 320  
 Gln Arg Trp Asp Ile Asn Glu Ile Asp Arg Leu Pro Asp Tyr Met Lys  
 325 330 335  
 Ile Ser Tyr Lys Ala Ile Leu Asp Leu Tyr Lys Asp Tyr Glu Lys Glu

T08290" 0282660

340 345 350  
 Leu Ser Ser Ala Gly Arg Ser His Ile Val Cys His Ala Ile Glu Arg  
 355 360 365  
 Met Lys Glu Val Val Arg Asn Tyr Asn Val Glu Ser Thr Trp Phe Ile  
 370 375 380  
 Glu Gly Tyr Met Pro Pro Val Ser Glu Tyr Leu Ser Asn Ala Leu Ala  
 385 390 395 400  
 Thr Thr Thr Tyr Tyr Tyr Leu Ala Thr Thr Ser Tyr Leu Gly Met Lys  
 405 410 415  
 Ser Ala Thr Glu Gln Asp Phe Glu Trp Leu Ser Lys Asn Pro Lys Ile  
 420 425 430  
 Leu Glu Ala Ser Val Ile Ile Cys Arg Val Ile Asp Asp Thr Ala Thr  
 435 440 445  
 Tyr Glu Val Glu Lys Ser Arg Gly Gln Ile Ala Thr Gly Ile Glu Cys  
 450 455 460  
 Cys Met Arg Asp Tyr Gly Ile Ser Thr Lys Glu Ala Met Ala Lys Phe  
 465 470 475 480  
 Gln Asn Met Ala Glu Thr Ala Trp Lys Asp Ile Asn Glu Gly Leu Leu  
 485 490 495  
 Arg Pro Thr Pro Val Ser Thr Glu Phe Leu Thr Pro Ile Leu Asn Leu  
 500 505 510  
 Ala Arg Ile Val Glu Val Thr Phe Ile His Asn Leu Asp Gly Tyr Thr  
 515 520 525  
 His Pro Glu Lys Val Leu Lys Pro His Ile Ile Asn Leu Leu Val Asp  
 530 535 540  
 Ser Ile Lys Ile  
 545

&lt;210&gt; 7

&lt;211&gt; 1644

&lt;212&gt; DNA

&lt;213&gt; Nicotiana tabacum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1644)

&lt;400&gt; 7

atg gcc tca gca gca gtt gca aac tat gaa gaa gag att gtt cgc ccc	48
Met Ala Ser Ala Ala Val Ala Asn Tyr Glu Glu Glu Ile Val Arg Pro	
1 5 10 15	
gtc gcc gac ttc tcc cct agt ctc tgg ggt gat cag ttc ctt tca ttc	96
Val Ala Asp Phe Ser Pro Ser Leu Trp Gly Asp Gln Phe Leu Ser Phe	
20 25 30	
tcc att gat aat cag gtt gcg gaa aag tat gct caa gag att gaa gca	144
Ser Ile Asp Asn Gln Val Ala Glu Lys Tyr Ala Gln Glu Ile Glu Ala	
35 40 45	
ttg aag gaa caa acg agg agt atg ctg tta gca acc gga agg aaa ttg	192
Leu Lys Glu Gln Thr Arg Ser Met Leu Leu Ala Thr Gly Arg Lys Leu	
50 55 60	
gcc gat aca ttg aat ttg att gac att att gaa cgc ctt ggt ata tcc	240
Ala Asp Thr Leu Asn Leu Ile Asp Ile Ile Glu Arg Leu Gly Ile Ser	
65 70 75 80	

tac cac ttt gag aaa gaa att gat gag att ttg gat cag att tac aac	288
Tyr His Phe Glu Lys Glu Ile Asp Glu Ile Leu Asp Gln Ile Tyr Asn	
85 90 95	
caa aac tca aac tgc aat gat ttg tgc acc tct gca ctt caa ttt cga	336
Gln Asn Ser Asn Cys Asn Asp Leu Cys Thr Ser Ala Leu Gln Phe Arg	
100 105 110	
ttg ctc agg caa cac ggt ttc aac atc tct cct gaa att ttc agc aaa	384
Leu Leu Arg Gln His Gly Phe Asn Ile Ser Pro Glu Ile Phe Ser Lys	
115 120 125	
ttc caa gat gaa aat ggc aaa ttc aag gag tct ctt gct agt gat gtc	432
Phe Gln Asp Glu Asn Gly Lys Phe Lys Glu Ser Leu Ala Ser Asp Val	
130 135 140	
tta gga tta tta aac ttg tat gaa gct tca cat gta agg act cat gct	480
Leu Gly Leu Leu Asn Leu Tyr Glu Ala Ser His Val Arg Thr His Ala	
145 150 155 160	
gac gat atc tta gaa gac gca ctt gct ttc tcc act atc cat ctt gaa	528
Asp Asp Ile Leu Glu Asp Ala Leu Ala Phe Ser Thr Ile His Leu Glu	
165 170 175	
tct gca gct cca cat ttg aaa tct cca ctt agg gag caa gtg aca cat	576
Ser Ala Ala Pro His Leu Lys Ser Pro Leu Arg Glu Gln Val Thr His	
180 185 190	
gcc ctt gag caa tgt ttg cac aag ggt gtt cct aga gtc gag acc cga	624
Ala Leu Glu Gln Cys Leu His Lys Gly Val Pro Arg Val Glu Thr Arg	
195 200 205	
ttc ttc atc tca tca atc tat gac aag gaa caa tcg aag aat aat gtg	672
Phe Phe Ile Ser Ser Ile Tyr Asp Lys Glu Gln Ser Lys Asn Asn Val	
210 215 220	
tta ctt cga ttt gcc aaa ttg gat ttc aac ttg ctc cag atg ttg cac	720
Leu Leu Arg Phe Ala Lys Leu Asp Phe Asn Leu Leu Gln Met Leu His	
225 230 235 240	
aaa caa gaa ctt gct caa gta tca agg tgg tgg aaa gat ttg gat ttt	768
Lys Gln Glu Leu Ala Gln Val Ser Arg Trp Trp Lys Asp Leu Asp Phe	
245 250 255	
gta aca aca ctt cca tat gct aga gat cga gta gtt gaa tgc tac ttt	816
Val Thr Thr Leu Pro Tyr Ala Arg Asp Arg Val Val Glu Cys Tyr Phe	
260 265 270	
tgg gca tta gga gtt tat ttt gag cct caa tac tct caa gct cgc gtc	864
Trp Ala Leu Gly Val Tyr Phe Glu Pro Gln Tyr Ser Gln Ala Arg Val	
275 280 285	
atg ctc gtt aag acc ata tca atg att tcg att gtc gat gac acc ttt	912
Met Leu Val Lys Thr Ile Ser Met Ile Ser Ile Val Asp Asp Thr Phe	
290 295 300	

gat gct tac ggt aca gtt aaa gaa ctt gag gca tac aca gat gcc ata	960
Asp Ala Tyr Gly Thr Val Lys Glu Leu Glu Ala Tyr Thr Asp Ala Ile	
305 310 315 320	
caa aga tgg gat atc aac gaa att gat cgg ctt cct gat tac atg aaa	1008
Gln Arg Trp Asp Ile Asn Glu Ile Asp Arg Leu Pro Asp Tyr Met Lys	
325 330 335	
atc agt tat aaa gct att cta gat ctc tac aag gat tat gaa aag gaa	1056
Ile Ser Tyr Lys Ala Ile Leu Asp Leu Tyr Lys Asp Tyr Glu Lys Glu	
340 345 350	
ttg tct agt gcc gga aga tct cat att gtc tgc cat gca ata gaa aga	1104
Leu Ser Ser Ala Gly Arg Ser His Ile Val Cys His Ala Ile Glu Arg	
355 360 365	
atg aaa gaa gta gta aga aat tat aat gtc gag tca aca tgg ttt att	1152
Met Lys Glu Val Val Arg Asn Tyr Asn Val Glu Ser Thr Trp Phe Ile	
370 375 380	
gaa gga tat atg cca cct gtt tct gaa tac cta agc aat gca cta gca	1200
Glu Gly Tyr Met Pro Pro Val Ser Glu Tyr Leu Ser Asn Ala Leu Ala	
385 390 395 400	
act acc aca tat tac tac ctc gcg aca aca tcg tat ttg ggc atg aag	1248
Thr Thr Thr Tyr Tyr Tyr Leu Ala Thr Thr Ser Tyr Leu Gly Met Lys	
405 410 415	
tct gcc acg gag caa gat ttt gag tgg ttg tca aag aat cca aaa att	1296
Ser Ala Thr Glu Gln Asp Phe Glu Trp Leu Ser Lys Asn Pro Lys Ile	
420 425 430	
ctt gaa gct agt gta att ata tgt cga gtt atc gat gac aca gcc acg	1344
Leu Glu Ala Ser Val Ile Ile Cys Arg Val Ile Asp Asp Thr Ala Thr	
435 440 445	
tac gag gtt gag aaa agc agg gga caa att gca act gga att gag tgc	1392
Tyr Glu Val Glu Lys Ser Arg Gly Gln Ile Ala Thr Gly Ile Glu Cys	
450 455 460	
tgc atg aga gat tat ggt ata tca aca aaa gag gca atg gct aaa ttt	1440
Cys Met Arg Asp Tyr Gly Ile Ser Thr Lys Glu Ala Met Ala Lys Phe	
465 470 475 480	
caa aat atg gct gag aca gca tgg aaa gat att aat gaa gga ctt ctt	1488
Gln Asn Met Ala Glu Thr Ala Trp Lys Asp Ile Asn Glu Gly Leu Leu	
485 490 495	
agg ccc act ccc gtc tct aca gaa ttt tta act cct att ctc aat ctt	1536
Arg Pro Thr Pro Val Ser Thr Glu Phe Leu Thr Pro Ile Leu Asn Leu	
500 505 510	
gct cgt att gtt gag gtt aca tat ata cac aat cta gat gga ttc act	1584
Ala Arg Ile Val Glu Val Thr Tyr Ile His Asn Leu Asp Gly Phe Thr	
515 520 525	
cat ccg gag aaa gtc tta aaa cct cac att att aac cta ctt gtg gac	1632

T02290"0226860

His Pro Glu Lys Val Leu Lys Pro His Ile Ile Asn Leu Leu Val Asp  
 530 535 540

tcc atc aaa att  
 Ser Ile Lys Ile  
 545

1644

<210> 8  
 <211> 548  
 <212> PRT  
 <213> Nicotiana tabacum

<400> 8

Met Ala Ser Ala Ala Val Ala Asn Tyr Glu Glu Glu Ile Val Arg Pro  
 1 5 10 15  
 Val Ala Asp Phe Ser Pro Ser Leu Trp Gly Asp Gln Phe Leu Ser Phe  
 20 25 30  
 Ser Ile Asp Asn Gln Val Ala Glu Lys Tyr Ala Gln Glu Ile Glu Ala  
 35 40 45  
 Leu Lys Glu Gln Thr Arg Ser Met Leu Leu Ala Thr Gly Arg Lys Leu  
 50 55 60  
 Ala Asp Thr Leu Asn Leu Ile Asp Ile Ile Glu Arg Leu Gly Ile Ser  
 65 70 75 80  
 Tyr His Phe Glu Lys Glu Ile Asp Glu Ile Leu Asp Gln Ile Tyr Asn  
 85 90 95  
 Gln Asn Ser Asn Cys Asn Asp Leu Cys Thr Ser Ala Leu Gln Phe Arg  
 100 105 110  
 Leu Leu Arg Gln His Gly Phe Asn Ile Ser Pro Glu Ile Phe Ser Lys  
 115 120 125  
 Phe Gln Asp Glu Asn Gly Lys Phe Lys Glu Ser Leu Ala Ser Asp Val  
 130 135 140  
 Leu Gly Leu Leu Asn Leu Tyr Glu Ala Ser His Val Arg Thr His Ala  
 145 150 155 160  
 Asp Asp Ile Leu Glu Asp Ala Leu Ala Phe Ser Thr Ile His Leu Glu  
 165 170 175  
 Ser Ala Ala Pro His Leu Lys Ser Pro Leu Arg Glu Gln Val Thr His  
 180 185 190  
 Ala Leu Glu Gln Cys Leu His Lys Gly Val Pro Arg Val Glu Thr Arg  
 195 200 205  
 Phe Phe Ile Ser Ser Ile Tyr Asp Lys Glu Gln Ser Lys Asn Asn Val  
 210 215 220  
 Leu Leu Arg Phe Ala Lys Leu Asp Phe Asn Leu Leu Gln Met Leu His  
 225 230 235 240  
 Lys Gln Glu Leu Ala Gln Val Ser Arg Trp Trp Lys Asp Leu Asp Phe  
 245 250 255  
 Val Thr Thr Leu Pro Tyr Ala Arg Asp Arg Val Val Glu Cys Tyr Phe  
 260 265 270  
 Trp Ala Leu Gly Val Tyr Phe Glu Pro Gln Tyr Ser Gln Ala Arg Val  
 275 280 285  
 Met Leu Val Lys Thr Ile Ser Met Ile Ser Ile Val Asp Asp Thr Phe  
 290 295 300  
 Asp Ala Tyr Gly Thr Val Lys Glu Leu Glu Ala Tyr Thr Asp Ala Ile  
 305 310 315 320  
 Gln Arg Trp Asp Ile Asn Glu Ile Asp Arg Leu Pro Asp Tyr Met Lys  
 325 330 335  
 Ile Ser Tyr Lys Ala Ile Leu Asp Leu Tyr Lys Asp Tyr Glu Lys Glu

F03290"0325850



```
<210> 9
<211> 1644
<212> DNA
<213> Nicotiana tabacum
```

```
<220>  
<221> CDS  
<222> (1) ... (1644)
```

<400>	9																
atg gcc tca gca gca gtt gca aac tat gaa gaa gag att gtt cgc ccc																	48
Met Ala Ser Ala Ala Val Ala Asn Tyr Glu Glu Glu Ile Val Arg Pro																	
1				5				10						15			
gtc gcc gac ttc tcc oct agt ctc tgg ggt gat cag ttc ctt tca ttc																	96
Val Ala Asp Phe Ser Pro Ser Leu Trp Gly Asp Gln Phe Leu Ser Phe																	
			20					25					30				
tcc att gat aat cag gtt gcg gaa aag tat gct caa gag att gaa gca																	144
Ser Ile Asp Asn Gln Val Ala Glu Lys Tyr Ala Gln Glu Ile Glu Ala																	
		35					40					45					
ttg aag gaa caa acg agg agt atg ctg tta gca acc gga agg aaa ttg																	192
Leu Lys Glu Gln Thr Arg Ser Met Leu Leu Ala Thr Gly Arg Lys Leu																	
	50					55				60							
gcc gat aca ttg aat ttg att gac att att gaa cgc ctt ggt ata tcc																	240
Ala Asp Thr Leu Asn Leu Ile Asp Ile Ile Glu Arg Leu Gly Ile Ser																	
65					70				75						80		

tac	cac	ttt	gag	aaa	gaa	att	gat	gag	att	ttg	gat	cag	att	tac	aac	288
Tyr	His	Phe	Glu	Lys	Glu	Ile	Asp	Glu	Ile	Leu	Asp	Gln	Ile	Tyr	Asn	
				85					90					95		
caa	aac	tca	aac	tgc	aat	gat	ttg	tgc	acc	tct	gca	ctt	caa	ttt	cga	336
Gln	Asn	Ser	Asn	Cys	Asn	Asp	Leu	Cys	Thr	Ser	Ala	Leu	Gln	Phe	Arg	
				100					105					110		
ttg	ctc	agg	caa	cac	ggt	ttc	aac	atc	tct	cct	gaa	att	ttc	agc	aaa	384
Leu	Leu	Arg	Gln	His	Gly	Phe	Asn	Ile	Ser	Pro	Glu	Ile	Phe	Ser	Lys	
				115					120					125		
ttc	caa	gat	gaa	aat	ggc	aaa	ttc	aag	gag	tct	ctt	gct	agt	gat	gtc	432
Phe	Gln	Asp	Glu	Asn	Gly	Lys	Phe	Lys	Glu	Ser	Leu	Ala	Ser	Asp	Val	
				130					135					140		
tta	gga	tta	tta	aac	ttg	tat	gaa	gct	tca	cat	gta	agg	act	cat	gct	480
Leu	Gly	Leu	Leu	Asn	Leu	Tyr	Glu	Ala	Ser	His	Val	Arg	Thr	His	Ala	
				145					150					155		
gac	gat	atc	tta	gaa	gac	gca	ctt	gct	ttc	toc	act	atc	cat	ctt	gaa	528
Asp	Asp	Ile	Leu	Glu	Asp	Ala	Leu	Ala	Phe	Ser	Thr	Ile	His	Leu	Glu	
				165					170					175		
tct	gca	gct	cca	cat	ttg	aaa	tct	cca	ctt	agg	gag	caa	gtg	aca	cat	576
Ser	Ala	Ala	Pro	His	Leu	Lys	Ser	Pro	Leu	Arg	Glu	Gln	Val	Thr	His	
				180					185					190		
gcc	ctt	gag	caa	tgt	ttg	cac	aag	ggt	ggt	cct	aga	gtc	gag	acc	cga	624
Ala	Leu	Glu	Gln	Cys	Leu	His	Lys	Gly	Val	Pro	Arg	Val	Glu	Thr	Arg	
				195					200					205		
ttc	ttc	atc	tca	tca	atc	tat	gac	aag	gaa	caa	tcg	aag	aat	aat	gtg	672
Phe	Phe	Ile	Ser	Ser	Ile	Tyr	Asp	Lys	Glu	Gln	Ser	Lys	Asn	Asn	Val	
				210					215					220		
tta	ctt	cga	ttt	gcc	aaa	ttg	gat	ttc	aac	ttg	ctc	cag	atg	ttg	cac	720
Leu	Leu	Arg	Phe	Ala	Lys	Leu	Asp	Phe	Asn	Leu	Leu	Gln	Met	Leu	His	
				225					230					235		
aaa	caa	gaa	ctt	gct	caa	gta	tca	agg	tgg	tgg	aaa	gat	ttg	gat	ttt	768
Lys	Gln	Glu	Leu	Ala	Gln	Val	Ser	Arg	Trp	Trp	Lys	Asp	Leu	Asp	Phe	
				245					250					255		
gta	aca	aca	ctt	cca	tat	gct	aga	gat	cga	gta	ggt	gaa	tgc	tac	ttt	816
Val	Thr	Thr	Leu	Pro	Tyr	Ala	Arg	Asp	Arg	Val	Val	Glu	Cys	Tyr	Phe	
				260					265					270		
tcg	gca	tta	gga	gtt	tat	ttt	gag	cct	caa	tac	tct	caa	gct	cgc	gtc	864
Ser	Ala	Leu	Gly	Val	Tyr	Phe	Glu	Pro	Gln	Tyr	Ser	Gln	Ala	Arg	Val	
				275					280					285		
atg	ctc	gtt	aag	acc	ata	tca	atg	att	tcg	att	gtc	gat	gac	acc	ttt	912
Met	Leu	Val	Lys	Thr	Ile	Ser	Met	Ile	Ser	Ile	Val	Asp	Asp	Thr	Phe	
				290					295					300		

gat gct tac ggt aca gtt aaa gaa ctt gag gca tac aca gat gcc ata	960
Asp Ala Tyr Gly Thr Val Lys Glu Leu Glu Ala Tyr Thr Asp Ala Ile	
305 310 315 320	
caa aga tgg gat atc aac gaa att gat cgg ctt cct gat tac atg aaa	1008
Gln Arg Trp Asp Ile Asn Glu Ile Asp Arg Leu Pro Asp Tyr Met Lys	
325 330 335	
atc agt tat aaa gct att cta gat ctc tac aag gat tat gaa aag gaa	1056
Ile Ser Tyr Lys Ala Ile Leu Asp Leu Tyr Lys Asp Tyr Glu Lys Glu	
340 345 350	
ttg tct agt gcc gga aga tct cat att gtc tgc cat gca ata gaa aga	1104
Leu Ser Ser Ala Gly Arg Ser His Ile Val Cys His Ala Ile Glu Arg	
355 360 365	
atg aaa gaa gta gta aga aat tat aat gtc gag tca aca tgg ttt att	1152
Met Lys Glu Val Val Arg Asn Tyr Asn Val Glu Ser Thr Trp Phe Ile	
370 375 380	
gaa gga tat atg cca cct gtt tct gaa tac cta agc aat gca cta gca	1200
Glu Gly Tyr Met Pro Pro Val Ser Glu Tyr Leu Ser Asn Ala Leu Ala	
385 390 395 400	
act acc aca tat tac tac ctc gcg aca aca tcg tat ttg ggc atg aag	1248
Thr Thr Thr Tyr Tyr Tyr Leu Ala Thr Thr Ser Tyr Leu Gly Met Lys	
405 410 415	
tct gcc acg gag caa gat ttt gag tgg ttg tca aag aat cca aaa att	1296
Ser Ala Thr Glu Gln Asp Phe Glu Trp Leu Ser Lys Asn Pro Lys Ile	
420 425 430	
ctt gaa gct agt gta att ata tgg cga gtt atc gat gac aca gcc acg	1344
Leu Glu Ala Ser Val Ile Ile Trp Arg Val Ile Asp Asp Thr Ala Thr	
435 440 445	
tac gag gtt gag aaa agc agg gga caa att gca act gga att gag tgc	1392
Tyr Glu Val Glu Lys Ser Arg Gly Gln Ile Ala Thr Gly Ile Glu Cys	
450 455 460	
tgc atg aga gat tat ggt ata tca aca aaa gag gca atg gct aaa ttt	1440
Cys Met Arg Asp Tyr Gly Ile Ser Thr Lys Glu Ala Met Ala Lys Phe	
465 470 475 480	
caa aat atg gct gag aca gca tgg aaa gat att aat gaa gga ctt ctt	1488
Gln Asn Met Ala Glu Thr Ala Trp Lys Asp Ile Asn Glu Gly Leu Leu	
485 490 495	
agg ccc act ccc gtc tct aca gaa ttt tta act cct att ctc aat ctt	1536
Arg Pro Thr Pro Val Ser Thr Glu Phe Leu Thr Pro Ile Leu Asn Leu	
500 505 510	
gct cgt att gtt gag gtt aca tat ata cac aat cta gat gga tac act	1584
Ala Arg Ile Val Glu Val Thr Tyr Ile His Asn Leu Asp Gly Tyr Thr	
515 520 525	
cat ccg gag aaa gtc tta aaa cct cac att att aac cta ctt gtg gac	1632

tcc atc aaa att  
Ser Ile Lys Ile  
545

1644

<400>	10															
Met	Ala	Ser	Ala	Ala	Val	Ala	Asn	Tyr	Glu	Glu	Glu	Ile	Val	Arg	Pro	
1				5					10					15		
Val	Ala	Asp	Phe	Ser	Pro	Ser	Leu	Trp	Gly	Asp	Gln	Phe	Leu	Ser	Phe	
		20						25					30			
Ser	Ile	Asp	Asn	Gln	Val	Ala	Glu	Lys	Tyr	Ala	Gln	Glu	Ile	Glu	Ala	
		35					40					45				
Leu	Lys	Glu	Gln	Thr	Arg	Ser	Met	Leu	Leu	Ala	Thr	Gly	Arg	Lys	Leu	
	50					55					60					
Ala	Asp	Thr	Leu	Asn	Leu	Ile	Asp	Ile	Ile	Glu	Arg	Leu	Gly	Ile	Ser	
65					70					75					80	
Tyr	His	Phe	Glu	Lys	Glu	Ile	Asp	Glu	Ile	Leu	Asp	Gln	Ile	Tyr	Asn	
				85					90					95		
Gln	Asn	Ser	Asn	Cys	Asn	Asp	Leu	Cys	Thr	Ser	Ala	Leu	Gln	Phe	Arg	
			100					105					110			
Leu	Leu	Arg	Gln	His	Gly	Phe	Asn	Ile	Ser	Pro	Glu	Ile	Phe	Ser	Lys	
		115					120					125				
Phe	Gln	Asp	Glu	Asn	Gly	Lys	Phe	Lys	Glu	Ser	Leu	Ala	Ser	Asp	Val	
	130				135						140					
Leu	Gly	Leu	Leu	Asn	Leu	Tyr	Glu	Ala	Ser	His	Val	Arg	Thr	His	Ala	
145				150						155					160	
Asp	Asp	Ile	Leu	Glu	Asp	Ala	Leu	Ala	Phe	Ser	Thr	Ile	His	Leu	Glu	
				165					170					175		
Ser	Ala	Ala	Pro	His	Leu	Lys	Ser	Pro	Leu	Arg	Glu	Gln	Val	Thr	His	
			180					185					190			
Ala	Leu	Glu	Gln	Cys	Leu	His	Lys	Gly	Val	Pro	Arg	Val	Glu	Thr	Arg	
		195					200					205				
Phe	Phe	Ile	Ser	Ser	Ile	Tyr	Asp	Lys	Glu	Gln	Ser	Lys	Asn	Asn	Val	
	210					215					220					
Leu	Leu	Arg	Phe	Ala	Lys	Leu	Asp	Phe	Asn	Leu	Leu	Gln	Met	Leu	His	
225					230					235					240	
Lys	Gln	Glu	Leu	Ala	Gln	Val	Ser	Arg	Trp	Trp	Lys	Asp	Leu	Asp	Phe	
				245					250					255		
Val	Thr	Thr	Leu	Pro	Tyr	Ala	Arg	Asp	Arg	Val	Val	Glu	Cys	Tyr	Phe	
			260					265					270			
Ser	Ala	Leu	Gly	Val	Tyr	Phe	Glu	Pro	Gln	Tyr	Ser	Gln	Ala	Arg	Val	
		275					280					285				
Met	Leu	Val	Lys	Thr	Ile	Ser	Met	Ile	Ser	Ile	Val	Asp	Asp	Thr	Phe	
	290					295					300					
Asp	Ala	Tyr	Gly	Thr	Val	Lys	Glu	Leu	Glu	Ala	Tyr	Thr	Asp	Ala	Ile	
					310					315					320	
Gln	Arg	Trp	Asp	Ile	Asn	Glu	Ile	Asp	Arg	Leu	Pro	Asp	Tyr	Met	Lys	
				325					3							

```
<210> 11
<211> 1644
<212> DNA
<213> Nicotiana tabacum
```

```
<220>  
<221> CDS  
<222> (1)...(1644)  
  
<221> misc_feature  
<222> (1)...(1644)  
<223> n = A,T,C or G
```

<400>	11																	
atg gcc tca gca gca gtt gca aac tat gaa gaa gag att gtt cgc ccc																	48	
Met Ala Ser Ala Ala Val Ala Asn Tyr Glu Glu Glu Ile Val Arg Pro																		
1					5				10						15			
<hr/>																		
gtc gcc gac ttc tcc cct agt ctc tgg ggt gat cag ttc ctt tca ttc																	96	
Val Ala Asp Phe Ser Pro Ser Leu Trp Gly Asp Gln Phe Leu Ser Phe																		
			20					25					30					
<hr/>																		
tcc att gat aat cag gtt gcg gaa aag tat gct caa gag att gaa gca																	144	
Ser Ile Asp Asn Gln Val Ala Glu Lys Tyr Ala Gln Glu Ile Glu Ala																		
		35					40					45						
<hr/>																		
ttg aag gaa caa acg agg agt atg ctg tta gca acc gga agg aaa ttg																	192	
Leu Lys Glu Gln Thr Arg Ser Met Leu Leu Ala Thr Gly Arg Lys Leu																		
50						55				60								

gcc gat aca ttg aat ttg att gac att att gaa cgc ctt ggt ata tcc	240
Ala Asp Thr Leu Asn Leu Ile Asp Ile Ile Glu Arg Leu Gly Ile Ser	
65 70 75 80	
tac cac ttt gag aaa gaa att gat gag att ttg gat cag att tac aac	288
Tyr His Phe Glu Lys Glu Ile Asp Glu Ile Leu Asp Gln Ile Tyr Asn	
85 90 95	
caa aac tca aac tgc aat gat ttg tgc acc tct gca ctt caa ttt cga	336
Gln Asn Ser Asn Cys Asn Asp Leu Cys Thr Ser Ala Leu Gln Phe Arg	
100 105 110	
ttg ctc agg caa cac ggt ttc aac atc tct cct gaa att ttc agc aaa	384
Leu Leu Arg Gln His Gly Phe Asn Ile Ser Pro Glu Ile Phe Ser Lys	
115 120 125	
ttc caa gat gaa aat ggc aaa ttc aag gag tct ctt gct agt gat gtc	432
Phe Gln Asp Glu Asn Gly Lys Phe Lys Glu Ser Leu Ala Ser Asp Val	
130 135 140	
tta gga tta tta aac ttg tat gaa gct tca cat gta agg act cat gct	480
Leu Gly Leu Leu Asn Leu Tyr Glu Ala Ser His Val Arg Thr His Ala	
145 150 155 160	
gac gat atc tta gaa gac gca ctt gct ttc tcc act atc cat ctt gaa	528
Asp Asp Ile Leu Glu Asp Ala Leu Ala Phe Ser Thr Ile His Leu Glu	
165 170 175	
tct gca gct cca cat ttg aaa tct cca ctt agg gag caa gtg aca cat	576
Ser Ala Ala Pro His Leu Lys Ser Pro Leu Arg Glu Gln Val Thr His	
180 185 190	
gcc ctt gag caa tgt ttg cac aag ggt gtt cct aga gtc gag acc cga	624
Ala Leu Glu Gln Cys Leu His Lys Gly Val Pro Arg Val Glu Thr Arg	
195 200 205	
ttc ttc atc tca tca atc tat gac aag gaa caa tcg aag aat aat gtg	672
Phe Phe Ile Ser Ser Ile Tyr Asp Lys Glu Gln Ser Lys Asn Asn Val	
210 215 220	
tta ctt cga ttt gcc aaa ttg gat ttc aac ttg ctc cag atg ttg cac	720
Leu Leu Arg Phe Ala Lys Leu Asp Phe Asn Leu Leu Gln Met Leu His	
225 230 235 240	
aaa caa gaa ctt gct caa gta tca agg tgg tgg aaa gat ttg gat ttt	768
Lys Gln Glu Leu Ala Gln Val Ser Arg Trp Trp Lys Asp Leu Asp Phe	
245 250 255	
gta aca aca ctt cca tat gct aga gat cga gta gtt gaa tgc tac ttt	816
Val Thr Thr Leu Pro Tyr Ala Arg Asp Arg Val Val Glu Cys Tyr Phe	
260 265 270	
tgg gca tta gga gtt tat ttt gag cct caa tac tct caa gct cgc gtc	864
Trp Ala Leu Gly Val Tyr Phe Glu Pro Gln Tyr Ser Gln Ala Arg Val	
275 280 285	

atg	ctc	gtt	aag	acc	ata	tca	atg	att	tcg	att	gtc	gat	gac	acc	ttt		912
Met	Leu	Val	Lys	Thr	Ile	Ser	Met	Ile	Ser	Ile	Val	Asp	Asp	Thr	Phe		
290295300																	
gat	gct	tac	ggt	aca	gtt	aaa	gaa	ctt	gag	gca	tac	aca	gat	gcc	ata		960
Asp	Ala	Tyr	Gly	Thr	Val	Lys	Glu	Leu	Glu	Ala	Tyr	Thr	Asp	Ala	Ile		
305310315320																	
caa	aga	tgg	gat	atc	aac	gaa	att	gat	cgg	ctt	cct	gat	tac	atg	aaa		1008
Gln	Arg	Trp	Asp	Ile	Asn	Glu	Ile	Asp	Arg	Leu	Pro	Asp	Tyr	Met	Lys		
325330335																	
atc	agt	tat	aaa	gct	att	cta	gat	ctc	tac	aag	gat	tat	gaa	aag	gaa		1056
Ile	Ser	Tyr	Lys	Ala	Ile	Leu	Asp	Leu	Tyr	Lys	Asp	Tyr	Glu	Lys	Glu		
340345350																	
ttg	tct	agt	gcc	gga	aga	tct	cat	att	gtc	tgc	cat	gca	ata	gaa	aga		1104
Leu	Ser	Ser	Ala	Gly	Arg	Ser	His	Ile	Val	Cys	His	Ala	Ile	Glu	Arg		
355360365																	
atg	aaa	gaa	gta	gta	aga	aat	tat	aat	gtc	gag	tca	aca	tgg	ttt	att		1152
Met	Lys	Glu	Val	Val	Arg	Asn	Tyr	Asn	Val	Glu	Ser	Thr	Trp	Phe	Ile		
370375380																	
gaa	gga	tat	atg	cca	cct	gtt	tct	gaa	tac	cta	agc	aat	gca	cta	gca		1200
Glu	Gly	Tyr	Met	Pro	Pro	Val	Ser	Glu	Tyr	Leu	Ser	Asn	Ala	Leu	Ala		
385390395400																	
act	acc	aca	tat	tac	nns	nns	gcg	aca	aca	tcg	tat	ttg	ggc	atg	aag		1248
Thr	Thr	Thr	Tyr	Tyr	Xaa	Xaa	Ala	Thr	Thr	Ser	Tyr	Leu	Gly	Met	Lys		
405410415																	
tct	gcc	acg	gag	caa	gat	ttt	gag	tgg	ttg	tca	aag	aat	cca	aaa	att		1296
Ser	Ala	Thr	Glu	Gln	Asp	Phe	Glu	Trp	Leu	Ser	Lys	Asn	Pro	Lys	Ile		
420425430																	
ctt	gaa	gct	agt	gta	att	ata	tgt	cga	gtt	atc	gat	gac	aca	gcc	acg		1344
Leu	Glu	Ala	Ser	Val	Ile	Ile	Cys	Arg	Val	Ile	Asp	Asp	Thr	Ala	Thr		
435440445																	
tac	gag	gtt	gag	aaa	agc	agg	gga	caa	att	gca	act	gga	att	gag	tgc		1392
Tyr	Glu	Val	Glu	Lys	Ser	Arg	Gly	Gln	Ile	Ala	Thr	Gly	Ile	Glu	Cys		
450455460																	
tgc	atg	aga	gat	tat	ggt	ata	tca	aca	aaa	gag	gca	atg	gct	aaa	ttt		1440
Cys	Met	Arg	Asp	Tyr	Gly	Ile	Ser	Thr	Lys	Glu	Ala	Met	Ala	Lys	Phe		
465470475480																	
caa	aat	atg	gct	gag	aca	gca	tgg	aaa	gat	att	aat	gaa	gga	ctt	ctt		1488
Gln	Asn	Met	Ala	Glu	Thr	Ala	Trp	Lys	Asp	Ile	Asn	Glu	Gly	Leu	Leu		
485490495																	
agg	ccc	act	ccc	gtc	tct	aca	gaa	ttt	tta	act	cct	att	ctc	aat	ctt		1536
Arg	Pro	Thr	Pro	Val	Ser	Thr	Glu	Phe	Leu	Thr	Pro	Ile	Leu	Asn	Leu		
500505510																	
gct	cgt	att	gtt	gag	gtt	aca	tat	ata	cac	aat	cta	gat	gga	tac	act		1584

<400>	12															
Met	Ala	Ser	Ala	Ala	Val	Ala	Asn	Tyr	Glu	Glu	Glu	Ile	Val	Arg	Pro	
1				5					10					15		
Val	Ala	Asp	Phe	Ser	Pro	Ser	Leu	Trp	Gly	Asp	Gln	Phe	Leu	Ser	Phe	
			20					25					30			
Ser	Ile	Asp	Asn	Gln	Val	Ala	Glu	Lys	Tyr	Ala	Gln	Glu	Ile	Glu	Ala	
		35					40					45				
Leu	Lys	Glu	Gln	Thr	Arg	Ser	Met	Leu	Leu	Ala	Thr	Gly	Arg	Lys	Leu	
	50					55					60					
Ala	Asp	Thr	Leu	Asn	Leu	Ile	Asp	Ile	Ile	Glu	Arg	Leu	Gly	Ile	Ser	
65					70					75					80	
Tyr	His	Phe	Glu	Lys	Glu	Ile	Asp	Glu	Ile	Leu	Asp	Gln	Ile	Tyr	Asn	
				85					90					95		
Gln	Asn	Ser	Asn	Cys	Asn	Asp	Leu	Cys	Thr	Ser	Ala	Leu	Gln	Phe	Arg	
			100					105					110			
Leu	Leu	Arg	Gln	His	Gly	Phe	Asn	Ile	Ser	Pro	Glu	Ile	Phe	Ser	Lys	
		115					120					125				
Phe	Gln	Asp	Glu	Asn	Gly	Lys	Phe	Lys	Glu	Ser	Leu	Ala	Ser	Asp	Val	
	130					135					140					
Leu	Gly	Leu	Leu	Asn	Leu	Tyr	Glu	Ala	Ser	His	Val	Arg	Thr	His	Ala	
145				150						155					160	
Asp	Asp	Ile	Leu	Glu	Asp	Ala	Leu	Ala	Phe	Ser	Thr	Ile	His	Leu	Glu	
				165					170					175		
Ser	Ala	Ala	Pro	His	Leu	Lys	Ser	Pro	Leu	Arg	Glu	Gln	Val	Thr	His	
			180					185					190			
Ala	Leu	Glu	Gln	Cys	Leu	His	Lys	Gly	Val	Pro	Arg	Val	Glu	Thr	Arg	
		195					200					205				
Phe	Phe	Ile	Ser	Ser	Ile	Tyr	Asp	Lys	Glu	Gln	Ser	Lys	Asn	Asn	Val	
	210					215					220					
Leu	Leu	Arg	Phe	Ala	Lys	Leu	Asp	Phe	Asn	Leu	Leu	Gln	Met	Leu	His	
225				230					235					240		
Lys	Gln	Glu	Leu	Ala	Gln	Val	Ser	Arg	Trp	Trp	Lys	Asp	Leu	Asp	Phe	
				245					250					255		
Val	Thr	Thr	Leu	Pro	Tyr	Ala	Arg	Asp	Arg	Val	Val	Glu	Cys	Tyr	Phe	
			260					265					270			



Trp Ala Leu Gly Val Tyr Phe Glu Pro Gln Tyr Ser Gln Ala Arg Val  
 275 280 285  
 Met Leu Val Lys Thr Ile Ser Met Ile Ser Ile Val Asp Asp Thr Phe  
 290 295 300  
 Asp Ala Tyr Gly Thr Val Lys Glu Leu Glu Ala Tyr Thr Asp Ala Ile  
 305 310 315 320  
 Gln Arg Trp Asp Ile Asn Glu Ile Asp Arg Leu Pro Asp Tyr Met Lys  
 325 330 335  
 Ile Ser Tyr Lys Ala Ile Leu Asp Leu Tyr Lys Asp Tyr Glu Lys Glu  
 340 345 350  
 Leu Ser Ser Ala Gly Arg Ser His Ile Val Cys His Ala Ile Glu Arg  
 355 360 365  
 Met Lys Glu Val Val Arg Asn Tyr Asn Val Glu Ser Thr Trp Phe Ile  
 370 375 380  
 Glu Gly Tyr Met Pro Pro Val Ser Glu Tyr Leu Ser Asn Ala Leu Ala  
 385 390 395 400  
 Thr Thr Thr Tyr Tyr Xaa Xaa Ala Thr Thr Ser Tyr Leu Gly Met Lys  
 405 410 415  
 Ser Ala Thr Glu Gln Asp Phe Glu Trp Leu Ser Lys Asn Pro Lys Ile  
 420 425 430  
 Leu Glu Ala Ser Val Ile Ile Cys Arg Val Ile Asp Asp Thr Ala Thr  
 435 440 445  
 Tyr Glu Val Glu Lys Ser Arg Gly Gln Ile Ala Thr Gly Ile Glu Cys  
 450 455 460  
 Cys Met Arg Asp Tyr Gly Ile Ser Thr Lys Glu Ala Met Ala Lys Phe  
 465 470 475 480  
 Gln Asn Met Ala Glu Thr Ala Trp Lys Asp Ile Asn Glu Gly Leu Leu  
 485 490 495  
 Arg Pro Thr Pro Val Ser Thr Glu Phe Leu Thr Pro Ile Leu Asn Leu  
 500 505 510  
 Ala Arg Ile Val Glu Val Thr Tyr Ile His Asn Leu Asp Gly Tyr Thr  
 515 520 525  
 His Pro Glu Lys Val Leu Lys Pro His Ile Ile Asn Leu Leu Val Asp  
 530 535 540  
 Ser Ile Lys Ile  
 545

<210> 13  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer for mutagenesis

<400> 13  
 gttgaatgct acttttcggc attaggagtt tat

33

<210> 14  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer for mutagenesis

<400> 14

T002290-02866660

33

<211> 33

<213> Artificial Sequence

<223> primer for mutagenesis

33

<211> 33

<213> Artificial Sequence

<223> primer for mutagenesis

33

<211> 54

<213> Artificial Sequence

<223> primer for mutagenesis

$\langle 222 \rangle$  (1) ... (54)

$\langle 223 \rangle$  n = A, T, C or G

54

<211> 54

### <213> Artificial Sequence

<223> primer for mutagenesis

 $\langle 222 \rangle \quad (1) \dots (54)$  $\langle 223 \rangle \quad n = A, T, C \text{ or } G$ 

54

<211> 2018

<212> DNA

$\langle 220 \rangle$ 

<222> (6)...(1889)

<223> pinene synthase

<400> 19

4007-15  
 cagca atg gct cta gtt tct acc gca cgg ttg gct tcc aaa tca tgc ctg 50  
 Met Ala Leu Val Ser Thr Ala Pro Leu Ala Ser Lys Ser Cys Leu  
 1 5 10 15

cac aaa tcg ttg atc agt tct acc cat gag ctt aag gct ctc tct aga 98  
 His Lys Ser Leu Ile Ser Ser Thr His Glu Leu Lys Ala Leu Ser Arg  
 20 25 30

aca att cca gct cta gga atg agt agg cga ggg aaa tct atc act cct 146  
Thr Ile Pro Ala Leu Gly Met Ser Arg Arg Gly Lys Ser Ile Thr Pro  
35 40 45

tcc atc agc atg agc tct acc acc gtt gta acc gat gat ggt gta cga 194  
Ser Ile Ser Met Ser Ser Thr Thr Val Val Thr Asp Asp Gly Val Arg  
50 55 60

aga cgc atg ggc gat ttc cat tcc aac ctc tgg gac gat gat gtc ata 242  
Arg Arg Met Gly Asp Phe His Ser Asn Leu Trp Asp Asp Asp Val Ile  
65 70 75

cag tct tta cca acg gct tat gag gaa aaa tcg tac ctg gag cgt gct 290  
Gln Ser Leu Pro Thr Ala Tyr Glu Glu Lys Ser Tyr Leu Glu Arg Ala  
80 85 90 95

gag aaa ctg atc ggg gaa gta aag aac atg ttc aat tcg atg tca tta 338  
Glu Lys Leu Ile Gly Glu Val Lys Asn Met Phe Asn Ser Met Ser Leu  
100 105 110

gaa gat gga gag tta atg agt ccg ctc aat gat ctc att caa cgc ctt 386  
Glu Asp Gly Glu Leu Met Ser Pro Leu Asn Asp Leu Ile Gln Arg Leu  
115 120 125

tgg	att	gtc	gac	agc	ctt	gaa	cgt	ttg	ggg	atc	cat	aga	cat	ttc	aaa	434
Trp	Ile	Val	Asp	Ser	Leu	Glu	Arg	Leu	Gly	Ile	His	Arg	His	Phe	Lys	
		130					135					140				

gat gag ata aaa tcg gcg ctt gat tat gtt tac agt tat tgg ggc gaa 482  
Asp Glu Ile Lys Ser Ala Leu Asp Tyr Val Tyr Ser Tyr Trp Gly Glu  
145 150 155

aat ggc atc gga tgc ggg agg gag agt gtt gtt act gat ctg aac tca 530  
Asn Gly Ile Gly Cys Gly Arg Glu Ser Val Val Thr Asp Leu Asn Ser  
160 165 170 175

act gcg ttg ggg ctt cga acc cta cga cta cac gga tac ccg gtg tct 578  
Thr Ala Leu Gly Leu Arg Thr Leu Arg Leu His Gly Tyr Pro Val Ser  
180 185 190

tca gat gtt ttc aaa gct ttc aaa ggc caa aat ggg cag ttt tcc tgc 626

Ser	Asp	Val	Phe	Lys	Ala	Phe	Lys	Gly	Gln	Asn	Gly	Gln	Phe	Ser	Cys	
			195					200					205			
tct	gaa	aat	att	cag	aca	gat	gaa	gag	atc	aga	ggc	gtt	ctg	aat	tta	674
Ser	Glu	Asn	Ile	Gln	Thr	Asp	Glu	Glu	Ile	Arg	Gly	Val	Leu	Asn	Leu	
		210					215					220				
ttc	cgg	gcc	tcc	ctc	att	gcc	ttt	cca	ggg	gag	aaa	att	atg	gat	gag	722
Phe	Arg	Ala	Ser	Leu	Ile	Ala	Phe	Pro	Gly	Glu	Lys	Ile	Met	Asp	Glu	
		225				230					235					
gct	gaa	atc	ttc	tct	acc	aaa	tat	tta	aaa	gaa	gcc	ctg	caa	aag	att	770
Ala	Glu	Ile	Phe	Ser	Thr	Lys	Tyr	Leu	Lys	Glu	Ala	Leu	Gln	Lys	Ile	
240					245					250					255	
ccg	gtc	tcc	agt	ctt	tcg	cga	gag	atc	ggg	gac	gtt	ttg	gaa	tat	ggt	818
Pro	Val	Ser	Ser	Leu	Ser	Arg	Glu	Ile	Gly	Asp	Val	Leu	Glu	Tyr	Gly	
				260					265					270		
tgg	cac	aca	tat	ttg	ccg	cga	ttg	gaa	gca	agg	aat	tac	atc	caa	gtc	866
Trp	His	Thr	Tyr	Leu	Pro	Arg	Leu	Glu	Ala	Arg	Asn	Tyr	Ile	Gln	Val	
			275					280					285			
ttt	gga	cag	gac	act	gag	aac	acg	aag	tca	tat	gtg	aag	agc	aaa	aaa	914
Phe	Gly	Gln	Asp	Thr	Glu	Asn	Thr	Lys	Ser	Tyr	Val	Lys	Ser	Lys	Lys	
		290					295					300				
ctt	tta	gaa	ctc	gca	aaa	ttg	gag	ttc	aac	atc	ttt	caa	tcc	tta	caa	962
Leu	Leu	Glu	Leu	Ala	Lys	Leu	Glu	Phe	Asn	Ile	Phe	Gln	Ser	Leu	Gln	
		305				310					315					
aag	agg	gag	tta	gaa	agt	ctg	gtc	aga	tgg	tgg	aaa	gaa	tcg	ggt	ttt	1010
Lys	Arg	Glu	Leu	Glu	Ser	Leu	Val	Arg	Trp	Trp	Lys	Glu	Ser	Gly	Phe	
320					325				330						335	
cct	gag	atg	acc	ttc	tgc	cga	cat	cgt	cac	gtg	gaa	tac	tac	act	ttg	1058
Pro	Glu	Met	Thr	Phe	Cys	Arg	His	Arg	His	Val	Glu	Tyr	Tyr	Thr	Leu	
				340					345					350		
gct	tcc	tgc	att	gcg	ttc	gag	cct	caa	cat	tct	gga	ttc	aga	ctc	ggc	1106
Ala	Ser	Cys	Ile	Ala	Phe	Glu	Pro	Gln	His	Ser	Gly	Phe	Arg	Leu	Gly	
			355					360					365			
ttt	gcc	aag	acg	tgt	cat	ctt	atc	acg	gtt	ctt	gac	gat	atg	tac	gac	1154
Phe	Ala	Lys	Thr	Cys	His	Leu	Ile	Thr	Val	Leu	Asp	Asp	Met	Tyr	Asp	
		370					375					380				
acc	ttc	ggc	aca	gta	gac	gag	ctg	gaa	ctc	ttc	aca	gcg	aca	atg	aag	1202
Thr	Phe	Gly	Thr	Val	Asp	Glu	Leu	Glu	Leu	Phe	Thr	Ala	Thr	Met	Lys	
		385				390					395					
aga	tgg	gat	ccg	tcc	tcg	ata	gat	tgc	ctt	cca	gaa	tat	atg	aaa	gga	1250
Arg	Trp	Asp	Pro	Ser	Ser	Ile	Asp	Cys	Leu	Pro	Glu					

				420				425				430							
gag	gag	gct	caa	ggc	cga	gat	acg	ctc	aca	tat	gct	cgg	gaa	gct	tgg	1346			
Glu	Glu	Ala	Gln	Gly	Arg	Asp	Thr	Leu	Thr	Tyr	Ala	Arg	Glu	Ala	Trp				
435				440				445											
gag	gct	tat	att	gat	tcg	tat	atg	caa	gaa	gca	agg	tgg	atc	gcc	act	1394			
Glu	Ala	Tyr	Ile	Asp	Ser	Tyr	Met	Gln	Glu	Ala	Arg	Trp	Ile	Ala	Thr				
450				455				460											
ggt	tac	ctg	ccc	tcc	ttt	gat	gag	tac	tac	gag	aat	ggg	aaa	gtt	agc	1442			
Gly	Tyr	Leu	Pro	Ser	Phe	Asp	Glu	Tyr	Tyr	Glu	Asn	Gly	Lys	Val	Ser				
465				470				475											
tgt	ggt	cat	cgc	ata	tcc	gca	ttg	caa	ccc	att	ctg	aca	atg	gac	atc	1490			
Cys	Gly	His	Arg	Ile	Ser	Ala	Leu	Gln	Pro	Ile	Leu	Thr	Met	Asp	Ile				
480				485				490											
ccc	ttt	cct	gat	cat	atc	ctc	aag	gaa	ggt	gac	ttc	cca	tca	aag	ctt	1538			
Pro	Phe	Pro	Asp	His	Ile	Leu	Lys	Glu	Val	Asp	Phe	Pro	Ser	Lys	Leu				
500				505				510											
aac	gac	ttg	gca	tgt	gcc	atc	ctt	cga	tta	cga	ggt	gat	acg	cgg	tgc	1586			
Asn	Asp	Leu	Ala	Cys	Ala	Ile	Leu	Arg	Leu	Arg	Gly	Asp	Thr	Arg	Cys				
515				520				525											
tac	aag	gcg	gac	agg	gct	cgt	gga	gaa	gaa	gct	tcc	tct	ata	tca	tgt	1634			
Tyr	Lys	Ala	Asp	Arg	Ala	Arg	Gly	Glu	Glu	Ala	Ser	Ser	Ile	Ser	Cys				
530				535				540											
tat	atg	aaa	gac	aat	cct	gga	gta	tca	gag	gaa	gat	gct	ctc	gat	cat	1682			
Tyr	Met	Lys	Asp	Asn	Pro	Gly	Val	Ser	Glu	Glu	Asp	Ala	Leu	Asp	His				
545				550				555											
atc	aac	gcc	atg	atc	agt	gac	gta	atc	aaa	gga	tta	aat	tgg	gaa	ctt	1730			
Ile	Asn	Ala	Met	Ile	Ser	Asp	Val	Ile	Lys	Gly	Leu	Asn	Trp	Glu	Leu				
560				565				570											
ctc	aaa	cca	gac	atc	aat	gtt	ccc	atc	tcg	gcg	aag	aaa	cat	gct	ttt	1778			
Leu	Lys	Pro	Asp	Ile	Asn	Val	Pro	Ile	Ser	Ala	Lys	Lys	His	Ala	Phe				
580				585				590											
gac	atc	gcc	aga	gct	ttc	cat	tac	ggc	tac	aaa	tac	cga	gac	ggc	tac	1826			
Asp	Ile	Ala	Arg	Ala	Phe	His	Tyr	Gly	Tyr	Lys	Tyr	Arg	Asp	Gly	Tyr				
595				600				605											
agc	gtt	gcc	aac	gtt	gaa	acg	aag	agt	ttg	gtc	acg	aga	acc	ctc	ctt	1874			
Ser	Val	Ala	Asn	Val	Glu	Thr	Lys	Ser	Leu	Val	Thr	Arg	Thr	Leu	Leu				
610				615				620											
gaa	tct	gtg	cct	ttg	tag	caacagctca	aatctatgcc	ctatgctatg								1922			
Glu	Ser	Val	Pro	Leu															
625																			
tcgggttaaaa	atatatgtgg	aaggtagccg	ttggatgtag	aggataagtt	tgttataatt												1982		
taataaaaqtt	qtaatttataa	aaaaaaaaaaaa	aaaaaa												2018				

<400> 20

Met	Ala	Leu	Val	Ser	Thr	Ala	Pro	Leu	Ala	Ser	Lys	Ser	Cys	Leu	His
1				5					10					15	
Lys	Ser	Leu	Ile	Ser	Ser	Thr	His	Glu	Leu	Lys	Ala	Leu	Ser	Arg	Thr
			20					25					30		
Ile	Pro	Ala	Leu	Gly	Met	Ser	Arg	Arg	Gly	Lys	Ser	Ile	Thr	Pro	Ser
		35					40					45			
Ile	Ser	Met	Ser	Ser	Thr	Thr	Val	Val	Thr	Asp	Asp	Gly	Val	Arg	Arg
	50					55					60				
Arg	Met	Gly	Asp	Phe	His	Ser	Asn	Leu	Trp	Asp	Asp	Asp	Val	Ile	Gln
65					70					75					80
Ser	Leu	Pro	Thr	Ala	Tyr	Glu	Glu	Lys	Ser	Tyr	Leu	Glu	Arg	Ala	Glu
				85					90					95	
Lys	Leu	Ile	Gly	Glu	Val	Lys	Asn	Met	Phe	Asn	Ser	Met	Ser	Leu	Glu
			100					105					110		
Asp	Gly	Glu	Leu	Met	Ser	Pro	Leu	Asn	Asp	Leu	Ile	Gln	Arg	Leu	Trp
		115					120					125			
Ile	Val	Asp	Ser	Leu	Glu	Arg	Leu	Gly	Ile	His	Arg	His	Phe	Lys	Asp
	130					135					140				
Glu	Ile	Lys	Ser	Ala	Leu	Asp	Tyr	Val	Tyr	Ser	Tyr	Trp	Gly	Glu	Asn
145					150					155					160
Gly	Ile	Gly	Cys	Gly	Arg	Glu	Ser	Val	Val	Thr	Asp	Leu	Asn	Ser	Thr
			165						170					175	
Ala	Leu	Gly	Leu	Arg	Thr	Leu	Arg	Leu	His	Gly	Tyr	Pro	Val	Ser	Ser
			180					185					190		
Asp	Val	Phe	Lys	Ala	Phe	Lys	Gly	Gln	Asn	Gly	Gln	Phe	Ser	Cys	Ser
		195					200					205			
Glu	Asn	Ile	Gln	Thr	Asp	Glu	Glu	Ile	Arg	Gly	Val	Leu	Asn	Leu	Phe
	210					215					220				
Arg	Ala	Ser	Leu	Ile	Ala	Phe	Pro	Gly	Glu	Lys	Ile	Met	Asp	Glu	Ala
225					230					235					240
Glu	Ile	Phe	Ser	Thr	Lys	Tyr	Leu	Lys	Glu	Ala	Leu	Gln	Lys	Ile	Pro
			245						250					255	
Val	Ser	Ser	Leu	Ser	Arg	Glu	Ile	Gly	Asp	Val	Leu	Glu	Tyr	Gly	Trp
			260					265					270		
His	Thr	Tyr	Leu	Pro	Arg	Leu	Glu	Ala	Arg	Asn	Tyr	Ile	Gln	Val	Phe
		275					280					285			
Gly	Gln	Asp	Thr	Glu	Asn	Thr	Lys	Ser	Tyr	Val	Lys	Ser	Lys	Lys	Leu
	290					295					300				
Leu	Glu	Leu	Ala	Lys	Leu	Glu	Phe	Asn	Ile	Phe	Gln	Ser	Leu	Gln	Lys
305					310					315					320
Arg	Glu	Leu	Glu	Ser	Leu	Val	Arg	Trp	Trp	Lys	Glu	Ser	Gly	Phe	Pro
				325					330					335	
Glu	Met	Thr	Phe	Cys	Arg	His	Arg	His	Val	Glu	Tyr	Tyr	Thr	Leu	Ala
			340					345					350		
Ser	Cys	Ile	Ala	Phe	Glu	Pro</									

```
<210> 21
<211> 2170
<212> DNA
<213> Mentha spicata

<220>
<221> CDS
<222> (29)...(1825)
<223> 4S-limonene synthase
```

<400>	21															52
agagagagag	aggaaggaaa	gattaatc	atg	gct	ctc	aaa	gtg	tta	agt	ggt						
			Met	Ala	Leu	Lys	Val	Leu	Ser	Val						
			1				5									
gca	act	caa	atg	gcg	att	cct	agc	aac	cta	acg	aca	tgt	ctt	caa	ccc	100
Ala	Thr	Gln	Met	Ala	Ile	Pro	Ser	Asn	Leu	Thr	Thr	Cys	Leu	Gln	Pro	
	10					15					20					
tca	cac	ttc	aaa	tct	tct	cca	aaa	ctg	tta	tct	agc	act	aac	agt	agt	148
Ser	His	Phe	Lys	Ser	Ser	Pro	Lys	Leu	Leu	Ser	Ser	Thr	Asn	Ser	Ser	
25					30					35					40	
agt	cgg	tct	cgc	ctc	cgt	gtg	tat	tgc	tcc	tcc	tcg	caa	ctc	act	act	196
Ser	Arg	Ser	Arg	Leu	Arg	Val	Tyr	Cys	Ser	Ser	Ser	Gln	Leu	Thr	Thr	
				45					50					55		

gaa Glu	aga Arg	cga Arg	tcc Ser	gga Gly	aac Asn	tac Tyr	aac Asn	cct Pro	tct Ser	cgt Arg	tgg Trp	gat Asp	gtc Val	aac Asn	ttc Phe	244
			60				65						70			
atc Ile	caa Gln	tcg Ser	ctt Leu	ctc Leu	agt Ser	gac Asp	tat Tyr	aag Lys	gag Glu	gac Asp	aaa Lys	cac His	gtg Val	att Ile	agg Arg	292
			75				80						85			
gct Ala	tct Ser	gag Glu	ctg Leu	gtc Val	act Thr	ttg Leu	gtg Val	aag Lys	atg Met	gaa Glu	ctg Leu	gag Glu	aaa Lys	gaa Glu	acg Thr	340
			90				95						100			
gat Asp	caa Gln	att Ile	cga Arg	caa Gln	ctt Leu	gag Glu	ttg Leu	atc Ile	gat Asp	gac Asp	ttg Leu	cag Gln	agg Arg	atg Met	ggg Gly	388
			105				110						115			120
ctg Leu	tcc Ser	gat Asp	cat His	ttc Phe	caa Gln	aat Asn	gag Glu	ttc Phe	aaa Lys	gaa Glu	atc Ile	ttg Leu	tcc Ser	tct Ser	ata Ile	436
			125				130						135			
tat Tyr	ctc Leu	gac Asp	cat His	cac His	tat Tyr	tac Tyr	aag Lys	aac Asn	cct Pro	ttt Phe	cca Pro	aaa Lys	gaa Glu	gaa Glu	agg Arg	484
			140				145						150			
gat Asp	ctc Leu	tac Tyr	tcc Ser	aca Thr	tct Ser	ctt Leu	gca Ala	ttt Phe	agg Arg	ctc Leu	ctc Leu	aga Arg	gaa Glu	cat His	ggt Gly	532
			155				160						165			
ttt Phe	caa Gln	gtc Val	gca Ala	caa Gln	gag Glu	gta Val	ttc Phe	gat Asp	agt Ser	ttc Phe	aag Lys	aac Asn	gag Glu	gag Glu	ggt Gly	580
			170				175						180			
gag Glu	ttc Phe	aaa Lys	gaa Glu	agc Ser	ctt Leu	agc Ser	gac Asp	gac Asp	acc Thr	aga Arg	gga Gly	ttg Leu	ttg Leu	caa Gln	ctg Leu	628
			185				190						195			200
tat Tyr	gaa Glu	gct Ala	tcc Ser	ttt Phe	ctg Leu	ttg Leu	acg Thr	gaa Glu	ggc Gly	gaa Glu	acc Thr	acg Thr	ctc Leu	gag Glu	tca Ser	676
			205				210						215			
gcg Ala	agg Arg	gaa Glu	ttc Phe	gcc Ala	acc Thr	aaa Lys	ttt Phe	ttg Leu	gag Glu	gaa Glu	aaa Lys	gtg Val	aac Asn	gag Glu	ggt Gly	724
			220				225						230			
ggt Gly	gtt Val	gat Asp	ggc Gly	gac Asp	ctt Leu	tta Leu	aca Thr	aga Arg	atc Ile	gca Ala	tat Tyr	tct Ser	ttg Leu	gac Asp	atc Ile	772
			235				240						245			
cct Pro	ctt Leu	cat His	tgg Trp	agg Arg	att Ile	aaa Lys	agg Arg	cca Pro	aat Asn	gca Ala	cct Pro	gtg Val	tgg Trp	atc Ile	gaa Glu	820
			250				255						260			
tgg Trp	tat Tyr	agg Arg	aag Lys	agg Arg	ccc Pro	gac Asp	atg Met	aat Asn	cca Pro	gta Val	gtg Val	ttg Leu	gag Glu	ctt Leu	gcc Ala	868
			265				270						275			280
ata Glu	ctc Arg	gac Asp	tta Leu	aat Asn	att Ile	gtt Leu	caa Gln	gca Ala	caa Gln	ttt Phe	caa Gln	gaa Glu	gag Glu	ctc Leu	aaa Gly	916





505					510						515					520	
tac	aat	gca	tcg	gag	gcg	gag	gcg	cgg	aag	cac	gtg	aaa	tgg	ctg	ata		1636
Tyr	Asn	Ala	Ser	Glu	Ala	Glu	Ala	Arg	Lys	His	Val	Lys	Trp	Leu	Ile		
				525					530					535			
gcg	gag	gtg	tgg	aag	aag	atg	aat	gcg	gag	agg	gtg	tcg	aag	gat	tct		1684
Ala	Glu	Val	Trp	Lys	Lys	Met	Asn	Ala	Glu	Arg	Val	Ser	Lys	Asp	Ser		
			540					545					550				
cca	ttc	ggc	aaa	gat	ttt	ata	gga	tgt	gca	gtt	gat	tta	gga	agg	atg		1732
Pro	Phe	Gly	Lys	Asp	Phe	Ile	Gly	Cys	Ala	Val	Asp	Leu	Gly	Arg	Met		
		555					560					565					
gcg	cag	ttg	atg	tac	cat	aat	gga	gat	ggg	cac	ggc	aca	caa	cac	cct		1780
Ala	Gln	Leu	Met	Tyr	His	Asn	Gly	Asp	Gly	His	Gly	Thr	Gln	His	Pro		
	570					575					580						
att	ata	cat	caa	caa	atg	acc	aga	acc	tta	ttc	gag	ccc	ttt	gca	tga		1828
Ile	Ile	His	Gln	Gln	Met	Thr	Arg	Thr	Leu	Phe	Glu	Pro	Phe	Ala			
585					590				595								
gagatgatga	cgagccatcg	tttacttact	taaattctac	caaagttttt	cgaaggcata												1888
gttcgtaatt	tttcaagcac	caataaataa	ggagaatcgg	ctcaaacaaa	cgtggcattt												1948
gccaccacgt	gagcacaagg	gagagtctgt	cgtcgtttat	ggatgaacta	ttcaattttt												2008
atgcatgtaa	taattaagtt	caagttcaag	agccttctgc	atattttaact	atgtattttga												2068
atttatcgag	tgtgattttc	tgtctttggc	aacatatatt	tttgtcatat	gtggcatcctt												2128
attatgatat	catacagtgt	ttatggatga	tatgatacta	tc													2170
<210> 22																	
<211> 599																	
<212> PRT																	
<213> Mentha spicata																	
<400> 22																	
Met	Ala	Leu	Lys	Val	Leu	Ser	Val	Ala	Thr	Gln	Met	Ala	Ile	Pro	Ser		
1				5				10						15			
Asn	Leu	Thr	Thr	Cys	Leu	Gln	Pro	Ser	His	Phe	Lys	Ser	Ser	Pro	Lys		
			20					25						30			
Leu	Leu	Ser	Ser	Thr	Asn	Ser	Ser	Ser	Arg	Ser	Arg	Leu	Arg	Val	Tyr		
		35					40					45					
Cys	Ser	Ser	Ser	Gln	Leu	Thr	Glu	Arg	Arg	Ser	Gly	Asn	Tyr	Asn			
50					55					60							
Pro	Ser	Arg	Trp	Asp	Val	Asn	Phe	Ile	Gln	Ser	Leu	Leu	Ser	Asp	Tyr		
65				70					75					80			
Lys	Glu	Asp	Lys	His	Val	Ile	Arg	Ala	Ser	Glu	Leu	Val	Thr	Leu	Val		
				85				90						95			
Lys	Met	Glu	Leu	Glu	Lys	Glu	Thr	Asp	Gln	Ile	Arg	Gln	Leu	Glu	Leu		
			100					105					110				
Ile	Asp	Asp	Leu	Gln													





gga ttg tta caa ttg tac gaa gct tcg ttt tta tca gca caa ggc gaa	627
Gly Leu Leu Gln Leu Tyr Glu Ala Ser Phe Leu Ser Ala Gln Gly Glu	
190 195 200 205	
gaa acc cta cat ctt gcc aga gat ttt gct act aaa ttt ctg cat aaa	675
Glu Thr Leu His Leu Ala Arg Asp Phe Ala Thr Lys Phe Leu His Lys	
210 215 220	
aga gta cta gtt gat aaa gac att aat ctc tta tca tca att gaa cgt	723
Arg Val Leu Val Asp Lys Asp Ile Asn Leu Leu Ser Ser Ile Glu Arg	
225 230 235	
gcg ttg gag ttg cct act cat tgg agg gtt caa atg ccc aac gca aga	771
Ala Leu Glu Leu Pro Thr His Trp Arg Val Gln Met Pro Asn Ala Arg	
240 245 250	
tcc ttc att gat gct tat aag agg aga ccc gac atg aat ccg act gtg	819
Ser Phe Ile Asp Ala Tyr Lys Arg Arg Pro Asp Met Asn Pro Thr Val	
255 260 265	
cta gaa cta gct aaa ttg gac ttc aat atg gtt caa gca caa ttt caa	867
Leu Glu Leu Ala Lys Leu Asp Phe Asn Met Val Gln Ala Gln Phe Gln	
270 275 280 285	
caa gag ctc aaa gag gcc tct agg tgg tgg aat agt acg ggt ctt gtc	915
Gln Glu Leu Lys Glu Ala Ser Arg Trp Trp Asn Ser Thr Gly Leu Val	
290 295 300	
cac gag ctt ccc ttt gtg aga gat agg att gtg gaa tgc tac tac tgg	963
His Glu Leu Pro Phe Val Arg Asp Arg Ile Val Glu Cys Tyr Tyr Trp	
305 310 315	
acg aca gga gtg gtt gag cgt cgt gaa cat gga tac gag agg ata atg	1011
Thr Thr Gly Val Val Glu Arg Arg Glu His Gly Tyr Glu Arg Ile Met	
320 325 330	
ctc acc aaa ata aat gct ctt gtt aca aca ata gac gat gtc ttt gat	1059
Leu Thr Lys Ile Asn Ala Leu Val Thr Thr Ile Asp Asp Val Phe Asp	
335 340 345	
att tat ggt acg ctt gaa gag cta caa cta ttc aca act gct att caa	1107
Ile Tyr Gly Thr Leu Glu Glu Leu Gln Leu Phe Thr Thr Ala Ile Gln	
350 355 360 365	
aga tgg gat att gaa tca atg aag caa ctc cct cct tac atg caa ata	1155
Arg Trp Asp Ile Glu Ser Met Lys Gln Leu Pro Pro Tyr Met Gln Ile	
370 375 380	
tgt tat ctt gct ctc ttc aac ttt gtg aat gag atg gct tat gat act	1203
Cys Tyr Leu Ala Leu Phe Asn Phe Val Asn Glu Met Ala Tyr Asp Thr	
385 390 395	
ctt agg gat aaa ggt ttc aac tcc acc cca tat cta cga aaa gcg tgg	1251
Leu Arg Asp Lys Gly Phe Asn Ser Thr Pro Tyr Leu Arg Lys Ala Trp	
400 405 410	
gtt gat ttg gtt gag tca tat cta ata gag gca aag tgg tac tac atg	1299

Val Asp Leu Val Glu Ser Tyr Leu Ile Glu Ala Lys Trp Tyr Tyr Met  
 415 420 425  
 gga cat aaa cct agt ttg gaa gaa tat atg aag aat agt tgg ata tca 1347  
 Gly His Lys Pro Ser Leu Glu Glu Tyr Met Lys Asn Ser Trp Ile Ser  
 430 435 440 445  
 atc gga ggc atc ccc att cta tct cat cta ttt ttc cgg cta aca gat 1395  
 Ile Gly Gly Ile Pro Ile Leu Ser His Leu Phe Phe Arg Leu Thr Asp  
 450 455 460  
 tcg att gag gaa gag gat gct gag agt atg cat aaa tac cat gat att 1443  
 Ser Ile Glu Glu Glu Asp Ala Glu Ser Met His Lys Tyr His Asp Ile  
 465 470 475  
 gtt cgt gca tcg tgt act att cta agg ctt gct gat gat atg gga aca 1491  
 Val Arg Ala Ser Cys Thr Ile Leu Arg Leu Ala Asp Asp Met Gly Thr  
 480 485 490  
 tcg ctg gat gag gtg gag aga ggc gac gtg ccc aaa tca gtt cag tgc 1539  
 Ser Leu Asp Glu Val Glu Arg Gly Asp Val Pro Lys Ser Val Gln Cys  
 495 500 505  
 tac atg aat gag aag aat gct tcg gaa gaa gaa gcg cga gag cat gtg 1587  
 Tyr Met Asn Glu Lys Asn Ala Ser Glu Glu Glu Ala Arg Glu His Val  
 510 515 520 525  
 cga tca ctc ata gac caa aca tgg aag atg atg aac aag gaa atg atg 1635  
 Arg Ser Leu Ile Asp Gln Thr Trp Lys Met Met Asn Lys Glu Met Met  
 530 535 540  
 acg tca tca ttt tcc aaa tat ttt gta caa gtt tct gct aat ctt gca 1683  
 Thr Ser Ser Phe Ser Lys Tyr Phe Val Gln Val Ser Ala Asn Leu Ala  
 545 550 555  
 aga atg gcg caa tgg ata tac cag cat gaa tct gat gga ttt ggc atg 1731  
 Arg Met Ala Gln Trp Ile Tyr Gln His Glu Ser Asp Gly Phe Gly Met  
 560 565 570  
 caa cat tca ttg gtg aac aaa atg ctc aga ggg ttg ttg ttc gac cgc 1779  
 Gln His Ser Leu Val Asn Lys Met Leu Arg Gly Leu Leu Phe Asp Arg  
 575 580 585  
 tat gag taa ctaatcttcg cccgggttcc aaatgaatca atctgttgtg 1828  
 Tyr Glu  
 590  
 ttgctgttcc acctgatatc aataataatt agacaaatgt ttctgtacgg gtggcccaac 1888  
 cgtcaggccc atttcgctca tgttcataat aaataataaaa actgttaatc aataacaaaa 1948  
 aaaaaaaaaa aaaaaaaaaa 1967

&lt;210&gt; 24

&lt;211&gt; 591

&lt;212&gt; PRT

&lt;213&gt; Salvia officinalis

&lt;400&gt; 24

T08220"00000000

Met 1	Ser	Ser	Leu	Ile 5	Met	Gln	Val	Val	Ile 10	Pro	Lys	Pro	Ala	Lys 15	Ile
Phe	His	Asn	Asn	Leu 20	Phe	Ser	Val	Ile 25	Ser	Lys	Arg	His	Arg	Phe	Ser
Thr	Thr	Ile 35	Thr	Thr	Arg	Gly	Gly 40	Arg	Trp	Ala	His	Cys 45	Ser	Leu	Gln
Met	Gly 50	Asn	Glu	Ile	Gln	Thr	Gly	Arg	Arg	Thr	Gly	Gly	Tyr	Gln	Pro
Thr 65	Leu	Trp	Asp	Phe 70	Ser	Thr	Ile	Gln	Leu	Phe	Asp	Ser	Glu	Tyr	Lys 80
Glu	Glu	Lys	His	Leu 85	Met	Arg	Ala	Ala	Gly 90	Met	Ile	Ala	Gln	Val	Asn 95
Met	Leu	Leu	Gln	Glu 100	Glu	Val	Asp	Ser	Ile	Gln	Arg	Leu	Glu	Leu	Ile
Asp	Asp	Leu 115	Arg	Arg	Leu	Gly	Ile 120	Ser	Cys	His	Phe	Asp	Arg	Glu	Ile
Val	Glu 130	Ile	Leu	Asn	Ser	Lys	Tyr 135	Tyr	Thr	Asn	Asn	Glu	Ile	Asp	Glu
Ser 145	Asp	Leu	Tyr	Ser	Thr	Ala	Leu	Arg	Phe	Lys	Leu	Leu	Arg	Gln	Tyr 160
Asp	Phe	Ser	Val	Ser 165	Gln	Glu	Val	Phe	Asp	Cys	Phe	Lys	Asn	Asp	Lys 175
Gly	Thr	Asp	Phe 180	Lys	Pro	Ser	Leu	Val	Asp	Asp	Thr	Arg	Gly	Leu	Leu
Gln	Leu	Tyr 195	Glu	Ala	Ser	Phe	Leu	Ser	Ala	Gln	Gly	Glu	Glu	Thr	Leu
His	Leu 210	Ala	Arg	Asp	Phe	Ala	Thr	Lys	Phe	Leu	His	Lys	Arg	Val	Leu
Val 225	Asp	Lys	Asp	Ile	Asn	Leu	Leu	Ser	Ser	Ile	Glu	Arg	Ala	Leu	Glu 240
Leu	Pro	Thr	His 245	Trp	Arg	Val	Gln	Met	Pro	Asn	Ala	Arg	Ser	Phe	Ile 255
Asp	Ala	Tyr	Lys 260	Arg	Arg	Pro	Asp	Met	Asn	Pro	Thr	Val	Leu	Glu	Leu
Ala	Lys	Leu	Asp 275	Phe	Asn	Met	Val	Gln	Ala	Gln	Phe	Gln	Gln	Glu	Leu
Lys	Glu 290	Ala	Ser	Arg	Trp	Trp	Asn	Ser	Thr	Gly	Leu	Val	His	Glu	Leu
Pro 305	Phe	Val	Arg	Asp	Arg	Ile	Val	Glu	Cys	Tyr	Tyr	Trp	Thr	Thr	Gly 320
Val	Val	Glu	Arg 325	Arg	Glu	His	Gly	Tyr	Glu	Arg	Ile	Met	Leu	Thr	Lys 335
Ile	Asn	Ala	Leu 340	Val	Thr	Thr	Ile	Asp	Asp	Val	Phe	Asp	Ile	Tyr	Gly
Thr	Leu	Glu 355	Glu	Leu	Gln	Leu	Phe	Thr	Thr	Ala	Ile	Gln	Arg	Trp	Asp
Ile	Glu 370	Ser	Met	Lys	Gln	Leu	Pro	Pro	Tyr	Met	Gln	Ile	Cys	Tyr	Leu
Ala 385	Leu	Phe	Asn	Phe	Val	Asn	Glu	Met	Ala	Tyr	Asp	Thr	Leu	Arg	Asp 400
Lys	Gly	Phe	Asn 405	Ser	Thr	Pro	Tyr	Leu	Arg	Lys	Ala	Trp	Val	Asp	Leu
Val	Glu	Ser	Tyr 420	Leu	Ile	Glu	Ala	Lys	Trp	Tyr	Tyr	Met	Gly	His	Lys
Pro	Ser	Leu 435	Glu	Glu	Tyr	Met	Lys	Asn	Ser	Trp	Ile	Ser	Ile	Gly	Gly
Ile	Pro	Ile	Leu	Ser	His	Leu	Phe	Phe	Arg	Leu	Thr	Asp	Ser	Ile	Glu

450		455		460	
Glu Glu Asp Ala Glu Ser Met His Lys Tyr His Asp Ile Val Arg Ala					
465		470		475	480
Ser Cys Thr Ile Leu Arg Leu Ala Asp Asp Met Gly Thr Ser Leu Asp					
	485		490		495
Glu Val Glu Arg Gly Asp Val Pro Lys Ser Val Gln Cys Tyr Met Asn					
	500		505		510
Glu Lys Asn Ala Ser Glu Glu Glu Ala Arg Glu His Val Arg Ser Leu					
	515		520		525
Ile Asp Gln Thr Trp Lys Met Met Asn Lys Glu Met Met Thr Ser Ser					
	530		535		540
Phe Ser Lys Tyr Phe Val Gln Val Ser Ala Asn Leu Ala Arg Met Ala					
545		550		555	560
Gln Trp Ile Tyr Gln His Glu Ser Asp Gly Phe Gly Met Gln His Ser					
	565		570		575
Leu Val Asn Lys Met Leu Arg Gly Leu Leu Phe Asp Arg Tyr Glu					
	580		585		590

&lt;210&gt; 25

&lt;211&gt; 2024

&lt;212&gt; DNA

<213> *Salvia officinalis*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (11)...(1804)

&lt;223&gt; (+)-bornyl diphosphate synthase

&lt;400&gt; 25

gatcacaaaa atg tct atc att agc atg aac gta tcg atc ctt agc aag	49
Met Ser Ile Ile Ser Met Asn Val Ser Ile Leu Ser Lys	
1 5 10	
cca cta aat tgc ctc cac aac ttg gag agg aga cct tca aaa gcc ttg	97
Pro Leu Asn Cys Leu His Asn Leu Glu Arg Arg Pro Ser Lys Ala Leu	
15 20 25	
ctt gtc cct tgc act gca ccc acc gct cgc ctc cgg gca tct tgc tcc	145
Leu Val Pro Cys Thr Ala Pro Thr Ala Arg Leu Arg Ala Ser Cys Ser	
30 35 40 45	
tca aaa cta caa gaa gct cat caa atc cga cga tct gga aac tac caa	193
Ser Lys Leu Gln Glu Ala His Gln Ile Arg Arg Ser Gly Asn Tyr Gln	
50 55 60	
cct gcc ctt tgg gat tcc aat tac att cag tct ctc aat act cca tat	241
Pro Ala Leu Trp Asp Ser Asn Tyr Ile Gln Ser Leu Asn Thr Pro Tyr	
65 70 75	
acg gag gag agg cac ttg gat aga aaa gca gag ctg att gtg caa gtg	289
Thr Glu Glu Arg His Leu Asp Arg Lys Ala Glu Leu Ile Val Gln Val	
80 85 90	
agg ata ctg cta aag gaa aaa atg gag cct gtt caa caa ttg gag ttg	337
Arg Ile Leu Leu Lys Glu Lys Met Glu Pro Val Gln Gln Leu Glu Leu	
95 100 105	

F08290.0236660



att cat gac ttg aaa tat ttg ggg ctc tcg gat ttt ttt caa gat gag	385
Ile His Asp Leu Lys Tyr Leu Gly Leu Ser Asp Phe Phe Gln Asp Glu	
110 115 120 125	
att aag gag atc tta ggt gtt ata tac aat gag cac aaa tgc ttt cac	433
Ile Lys Glu Ile Leu Gly Val Ile Tyr Asn Glu His Lys Cys Phe His	
130 135 140	
aat aat gaa gta gag aaa atg gat ttg tat ttc aca gct ctt gga ttc	481
Asn Asn Glu Val Glu Lys Met Asp Leu Tyr Phe Thr Ala Leu Gly Phe	
145 150 155	
aga ctc ctc aga caa cat ggt ttt aat att tcc caa gat gta ttt aat	529
Arg Leu Leu Arg Gln His Gly Phe Asn Ile Ser Gln Asp Val Phe Asn	
160 165 170	
tgt ttc aag aac gag aag ggt att gat ttc aag gca agc ctt gct caa	577
Cys Phe Lys Asn Glu Lys Gly Ile Asp Phe Lys Ala Ser Leu Ala Gln	
175 180 185	
gat acg aag gga atg tta caa ctg tat gaa gcg tct ttc ctt ttg aga	625
Asp Thr Lys Gly Met Leu Gln Leu Tyr Glu Ala Ser Phe Leu Leu Arg	
190 195 200 205	
aaa ggt gaa gat aca ttg gag ctt gca aga gaa ttt gcc aca aaa tgt	673
Lys Gly Glu Asp Thr Leu Glu Leu Ala Arg Glu Phe Ala Thr Lys Cys	
210 215 220	
ctg cag aaa aaa ctt gat gaa ggt ggt aat gaa att gat gag aat cta	721
Leu Gln Lys Lys Leu Asp Glu Gly Gly Asn Glu Ile Asp Glu Asn Leu	
225 230 235	
tta ttg tgg att cgc cac tct ttg gat ctt cct ctc cac tgg agg att	769
Leu Leu Trp Ile Arg His Ser Leu Asp Leu Pro Leu His Trp Arg Ile	
240 245 250	
caa agt gta gag gca aga tgg ttc ata gat gct tat gcg aga agg cca	817
Gln Ser Val Glu Ala Arg Trp Phe Ile Asp Ala Tyr Ala Arg Arg Pro	
255 260 265	
gac atg aat cca ctt att ttc gag ctt gcc aaa ctc aac ttc aat att	865
Asp Met Asn Pro Leu Ile Phe Glu Leu Ala Lys Leu Asn Phe Asn Ile	
270 275 280 285	
att caa gca aca cat caa caa gaa ctg aaa gat ctc tcg agg tgg tgg	913
Ile Gln Ala Thr His Gln Gln Glu Leu Lys Asp Leu Ser Arg Trp Trp	
290 295 300	
agt aga tta tgc ttc cct gaa aag ctc cca ttt gtg agg gat agg ctc	961
Ser Arg Leu Cys Phe Pro Glu Lys Leu Pro Phe Val Arg Asp Arg Leu	
305 310 315	
gtt gaa tcc ttc ttt tgg gcg gtt ggg atg ttt gag cca cat caa cat	1009
Val Glu Ser Phe Phe Trp Ala Val Gly Met Phe Glu Pro His Gln His	
320 325 330	
gga tat cag aga aaa atg gcc gcc aca att att gtt tta gca aca gtt	1057

Gly Tyr Gln Arg Lys Met Ala Ala Thr Ile Ile Val Leu Ala Thr Val	
335 340 345	
ata gat gat att tac gat gtg tat ggt aca cta gat gaa cta gaa cta	1105
Ile Asp Asp Ile Tyr Asp Val Tyr Gly Thr Leu Asp Glu Leu Glu Leu	
350 355 360 365	
ttt aca gac acg ttt aag aga tgg gat act gaa tca ata acc cga ctt	1153
Phe Thr Asp Thr Phe Lys Arg Trp Asp Thr Glu Ser Ile Thr Arg Leu	
370 375 380	
cct tat tac atg caa tta tgt tat tgg ggt gtc cac aac tat att tcc	1201
Pro Tyr Tyr Met Gln Leu Cys Tyr Trp Gly Val His Asn Tyr Ile Ser	
385 390 395	
gat gca gca tat gat att ctc aaa gaa cat ggt ttc ttt tgt ctc caa	1249
Asp Ala Ala Tyr Asp Ile Leu Lys Glu His Gly Phe Phe Cys Leu Gln	
400 405 410	
tat ctc cgg aaa tcg gtg gta gat ttg gtt gaa gca tat ttt cac gag	1297
Tyr Leu Arg Lys Ser Val Val Asp Leu Val Glu Ala Tyr Phe His Glu	
415 420 425	
gca aag tgg tac cac agc ggt tat aca cca agc ctg gat gaa tat ctc	1345
Ala Lys Trp Tyr His Ser Gly Tyr Thr Pro Ser Leu Asp Glu Tyr Leu	
430 435 440 445	
aac atc gcc aag att tca gtg gcg tct cct gca ata ata tcc cca acc	1393
Asn Ile Ala Lys Ile Ser Val Ala Ser Pro Ala Ile Ile Ser Pro Thr	
450 455 460	
tat ttc aca ttc gca aac gcg tct cat gac aca gca gtc atc gac agc	1441
Tyr Phe Thr Phe Ala Asn Ala Ser His Asp Thr Ala Val Ile Asp Ser	
465 470 475	
ttg tac caa tat cat gac ata ctt tgc cta gca gga att att ttg agg	1489
Leu Tyr Gln Tyr His Asp Ile Leu Cys Leu Ala Gly Ile Ile Leu Arg	
480 485 490	
ctt ccc gac gat ctt ggg aca tca tat ttt gag ctg gcg aga ggc gac	1537
Leu Pro Asp Asp Leu Gly Thr Ser Tyr Phe Glu Leu Ala Arg Gly Asp	
495 500 505	
gtg ccg aaa aca atc cag tgc tac atg aag gaa aca aat gct agt gag	1585
Val Pro Lys Thr Ile Gln Cys Tyr Met Lys Glu Thr Asn Ala Ser Glu	
510 515 520 525	
gag gag gcg gtg gag cac gtg aag ttt ctg ata agg gag gcg tgg aag	1633
Glu Glu Ala Val Glu His Val Lys Phe Leu Ile Arg Glu Ala Trp Lys	
530 535 540	
gat atg aac acg gcc ata gca gcc ggt tat ccg ttt ccg gat ggt atg	1681
Asp Met Asn Thr Ala Ile Ala Ala Gly Tyr Pro Phe Pro Asp Gly Met	
545 550 555	
gtg gcg ggc gca gct aat att ggg cgc gtg gcg cag ttt att tat ctc	1729
Val Ala Gly Ala Ala Asn Ile Gly Arg Val Ala Gln Phe Ile Tyr Leu	

```
<210> 26
<211> 598
<212> PRT
<213> Salvia officinalis
```

<400>	26														
Met	Ser	Ile	Ile	Ser	Met	Asn	Val	Ser	Ile	Leu	Ser	Lys	Pro	Leu	Asn
1				5					10					15	
Cys	Leu	His	Asn	Leu	Glu	Arg	Arg	Pro	Ser	Lys	Ala	Leu	Leu	Val	Pro
			20					25					30		
Cys	Thr	Ala	Pro	Thr	Ala	Arg	Leu	Arg	Ala	Ser	Cys	Ser	Ser	Lys	Leu
		35					40					45			
Gln	Glu	Ala	His	Gln	Ile	Arg	Arg	Ser	Gly	Asn	Tyr	Gln	Pro	Ala	Leu
	50					55					60				
Trp	Asp	Ser	Asn	Tyr	Ile	Gln	Ser	Leu	Asn	Thr	Pro	Tyr	Thr	Glu	Glu
65				70						75					80
Arg	His	Leu	Asp	Arg	Lys	Ala	Glu	Leu	Ile	Val	Gln	Val	Arg	Ile	Leu
				85					90					95	
Leu	Lys	Glu	Lys	Met	Glu	Pro	Val	Gln	Gln	Leu	Glu	Leu	Ile	His	Asp
			100					105					110		
Leu	Lys	Tyr	Leu	Gly	Leu	Ser	Asp	Phe	Phe	Gln	Asp	Glu	Ile	Lys	Glu
		115					120					125			
Ile	Leu	Gly	Val	Ile	Tyr	Asn	Glu	His	Lys	Cys	Phe	His	Asn	Asn	Glu
	130					135					140				
Val	Glu	Lys	Met	Asp	Leu	Tyr	Phe	Thr	Ala	Leu	Gly	Phe	Arg	Leu	Leu
145				150						155					160
Arg	Gln	His	Gly	Phe	Asn	Ile	Ser	Gln	Asp	Val	Phe	Asn	Cys	Phe	Lys
				165					170					175	
Asn	Glu	Lys	Gly	Ile	Asp	Phe	Lys	Ala	Ser	Leu	Ala	Gln	Asp	Thr	Lys
			180					185					190		
Gly	Met	Leu	Gln	Leu	Tyr	Glu	Ala	Ser	Phe	Leu	Leu	Arg	Lys	Gly	Glu
	195						200					205			
Asp	Thr	Leu	Glu	Leu	Ala	Arg	Glu	Phe	Ala	Thr	Lys	Cys	Leu	Gln	Lys
	210					215					220				
Lys	Leu	Asp	Glu	Gly	Gly	Asn	Glu	Ile	Asp	Glu	Asn	Leu	Leu	Leu	Trp
225				230						235					240
Ile	Arg	His	Ser	Leu	Asp	Leu	Pro	Leu	His	Trp	Arg	Ile	Gln	Ser	Val
				245					250					255	
Glu	Ala	Arg	Trp	Phe	Ile	Asp	Ala	Tyr	Ala	Arg	Arg	Pro	Asp	Met	Asn
			260					265					270		
Pro	Leu	Ile	Phe	Glu	Leu	Ala	Lys	Leu	Asn	Phe	Asn	Ile	Ile	Gln	Ala
		275					280					285			

Thr His Gln Gln Glu Leu Lys Asp Leu Ser Arg Trp Trp Ser Arg Leu  
 290 295 300  
 Cys Phe Pro Glu Lys Leu Pro Phe Val Arg Asp Arg Leu Val Glu Ser  
 305 310 315 320  
 Phe Phe Trp Ala Val Gly Met Phe Glu Pro His Gln His Gly Tyr Gln  
 325 330 335  
 Arg Lys Met Ala Ala Thr Ile Ile Val Leu Ala Thr Val Ile Asp Asp  
 340 345 350  
 Ile Tyr Asp Val Tyr Gly Thr Leu Asp Glu Leu Glu Leu Phe Thr Asp  
 355 360 365  
 Thr Phe Lys Arg Trp Asp Thr Glu Ser Ile Thr Arg Leu Pro Tyr Tyr  
 370 375 380  
 Met Gln Leu Cys Tyr Trp Gly Val His Asn Tyr Ile Ser Asp Ala Ala  
 385 390 395 400  
 Tyr Asp Ile Leu Lys Glu His Gly Phe Phe Cys Leu Gln Tyr Leu Arg  
 405 410 415  
 Lys Ser Val Val Asp Leu Val Glu Ala Tyr Phe His Glu Ala Lys Trp  
 420 425 430  
 Tyr His Ser Gly Tyr Thr Pro Ser Leu Asp Glu Tyr Leu Asn Ile Ala  
 435 440 445  
 Lys Ile Ser Val Ala Ser Pro Ala Ile Ile Ser Pro Thr Tyr Phe Thr  
 450 455 460  
 Phe Ala Asn Ala Ser His Asp Thr Ala Val Ile Asp Ser Leu Tyr Gln  
 465 470 475 480  
 Tyr His Asp Ile Leu Cys Leu Ala Gly Ile Ile Leu Arg Leu Pro Asp  
 485 490 495  
 Asp Leu Gly Thr Ser Tyr Phe Glu Leu Ala Arg Gly Asp Val Pro Lys  
 500 505 510  
 Thr Ile Gln Cys Tyr Met Lys Glu Thr Asn Ala Ser Glu Glu Glu Ala  
 515 520 525  
 Val Glu His Val Lys Phe Leu Ile Arg Glu Ala Trp Lys Asp Met Asn  
 530 535 540  
 Thr Ala Ile Ala Ala Gly Tyr Pro Phe Pro Asp Gly Met Val Ala Gly  
 545 550 555 560  
 Ala Ala Asn Ile Gly Arg Val Ala Gln Phe Ile Tyr Leu His Gly Asp  
 565 570 575  
 Gly Phe Gly Val Gln His Ser Lys Thr Tyr Glu His Ile Ala Gly Leu  
 580 585 590  
 Leu Phe Glu Pro Tyr Ala  
 595

<210> 27

<211> 1959

<212> DNA

<213> Mentha x piperita

<220>

<221> CDS

<222> (71)...(1720)

<223> (E)-B-farnesene synthase

<400> 27

aaactctgca atttcatata taacatcata aaatcagaga gagagacaga gagtttgttg

tagtgaaaaa atg gct aca aac ggc gtc gta att agt tgc tta agg gaa

Met Ala Thr Asn Gly Val Val Ile Ser Cys Leu Arg Glu

1

5

10

60

109

gta Val	agg Arg	cca Pro	cct Pro	atg Met	acg Thr	aag Lys	cat His	gcg Ala	cca Pro	agc Ser	atg Met	tgg Trp	act Thr	gat Asp	acc Thr	157
15						20			25							
ttt Phe	tct Ser	aac Asn	ttt Phe	tct Ser	ctt Leu	gac Asp	gat Asp	aag Lys	gaa Glu	caa Gln	caa Gln	aag Lys	tgc Cys	tca Ser	gaa Glu	205
30			35			40						45				
acc Thr	atc Ile	gaa Glu	gca Ala	ctt Leu	aag Lys	caa Gln	gaa Glu	gca Ala	aga Arg	ggc Gly	atg Met	ctt Leu	atg Met	gct Ala	gca Ala	253
				50		55								60		
acc Thr	act Thr	cct Pro	ctc Leu	caa Gln	caa Gln	atg Met	aca Thr	cta Leu	atc Ile	gac Asp	act Thr	ctc Leu	gag Glu	cgt Arg	ttg Leu	301
			65					70					75			
gga Gly	ttg Leu	tct Ser	ttc Phe	cat His	ttt Phe	gag Glu	acg Thr	gag Glu	atc Ile	gaa Glu	tac Tyr	aaa Lys	atc Ile	gaa Glu	cta Leu	349
80						85						90				
atc Ile	aac Asn	gct Ala	gca Ala	gaa Glu	gac Asp	gac Asp	ggc Gly	ttt Phe	gat Asp	ttg Leu	ttc Phe	gct Ala	act Thr	gct Ala	ctt Leu	397
95						100			105							
cgt Arg	ttc Phe	cgt Arg	ttg Leu	ctc Leu	aga Arg	caa Gln	cat His	caa Gln	cgc Arg	cac His	gtt Val	tct Ser	tgt Cys	gat Asp	gtt Val	445
110			115			120			125							
ttc Phe	gac Asp	aag Lys	ttc Phe	atc Ile	gac Asp	aaa Lys	gat Asp	ggc Gly	aag Lys	ttc Phe	gaa Glu	gaa Glu	tcc Ser	ctt Leu	agc Ser	493
			130			135						140				
aat Asn	aat Asn	gtt Val	gaa Glu	ggc Gly	cta Leu	tta Leu	agc Ser	ttg Leu	tat Tyr	gaa Glu	gca Ala	gct Ala	cat His	gtt Val	ggg Gly	541
145						150						155				
ttt Phe	cgc Arg	gaa Glu	gaa Glu	aga Arg	ata Ile	tta Leu	caa Gln	gag Glu	gct Ala	gta Val	aat Asn	ttt Phe	acg Thr	agg Arg	cat His	589
160						165						170				
cac His	ttg Leu	gaa Glu	gga Gly	gca Ala	gag Glu	tta Leu	gat Asp	cag Gln	tct Ser	cca Pro	tta Leu	ttg Leu	att Ile	aga Arg	gag Glu	637
175			180			185										
aaa Lys	gtg Val	aag Lys	cga Arg	gct Ala	ttg Leu	gag Glu	cac His	cct Pro	ctt Leu	cat His	agg Arg	gat Asp	ttc Phe	ccc Pro	att Ile	685
190			195			200						205				
gtc Val	tat Tyr	gca Ala	cgc Arg	ctt Leu	ttc Phe	atc Ile	tcc Ser	att Ile	tac Tyr	gaa Glu	aag Lys	gat Asp	gac Asp	tct Ser	aga Arg	733
			210						215			220				
gat Asp	gaa Glu	tta Leu	ctt Leu	ctc Leu	aag Lys	cta Leu	tcc Ser	aaa Lys	gtc Val	aac Asn	ttc Phe	aaa Lys	ttc Phe	atg Met	cag Gln	781
			225			230						235				
aat Asn	ttg Leu	tat Val	aag Glu	gaa Glu	gag Glu	ctc Leu	tcc Ser	caa Gln	ctc Leu	tcc Glu	agg Arg	tgg Trp	tgg Trp	aac Asn	aca Glu	829

Asn	Leu	Tyr	Lys	Glu	Glu	Leu	Ser	Gln	Leu	Ser	Arg	Trp	Trp	Asn	Thr	
		240					245					250				
tgg	aat	ctg	aaa	tca	aaa	tta	cca	tat	gca	aga	gat	cga	gtc	gtg	gag	877
Trp	Asn	Leu	Lys	Ser	Lys	Leu	Pro	Tyr	Ala	Arg	Asp	Arg	Val	Val	Glu	
		255					260				265					
gct	tat	gtt	tgg	gga	gta	ggg	tac	cat	tac	gaa	ccc	caa	tac	tca	tat	925
Ala	Tyr	Val	Trp	Gly	Val	Gly	Tyr	His	Tyr	Glu	Pro	Gln	Tyr	Ser	Tyr	
							275				280				285	
gtt	cga	atg	gga	ctt	gcc	aaa	ggc	gta	cta	att	tgt	gga	atc	atg	gac	973
Val	Arg	Met	Gly	Leu	Ala	Lys	Gly	Val	Leu	Ile	Cys	Gly	Ile	Met	Asp	
											295				300	
gat	aca	tat	gat	aat	tat	gct	aca	ctc	aat	gaa	gct	caa	ctt	ttt	act	1021
Asp	Thr	Tyr	Asp	Asn	Tyr	Ala	Thr	Leu	Asn	Glu	Ala	Gln	Leu	Phe	Thr	
			305					310					315			
caa	gtc	tta	gac	aag	tgg	gat	aga	gat	gaa	gct	gaa	cga	ctc	cca	gaa	1069
Gln	Val	Leu	Asp	Lys	Trp	Asp	Arg	Asp	Glu	Ala	Glu	Arg	Leu	Pro	Glu	
												330				
		320					325									
tac	atg	aaa	atc	gtt	tat	cga	ttt	att	ttg	agt	ata	tat	gaa	aat	tat	1117
Tyr	Met	Lys	Ile	Val	Tyr	Arg	Phe	Ile	Leu	Ser	Ile	Tyr	Glu	Asn	Tyr	
		335					340				345					
gaa	cgt	gat	gca	gcg	aaa	ctt	gga	aaa	agc	ttt	gca	gct	cct	tat	ttt	1165
Glu	Arg	Asp	Ala	Ala	Lys	Leu	Gly	Lys	Ser	Phe	Ala	Ala	Pro	Tyr	Phe	
							355				360				365	
aag	gaa	acc	gtg	aaa	caa	ctg	gca	agg	gca	ttt	aat	gag	gag	cag	aag	1213
Lys	Glu	Thr	Val	Lys	Gln	Leu	Ala	Arg	Ala	Phe	Asn	Glu	Glu	Gln	Lys	
			370							375					380	
tgg	gtt	atg	gaa	agg	cag	cta	ccg	tca	ttc	caa	gac	tac	gta	aag	aat	1261
Trp	Val	Met	Glu	Arg	Gln	Leu	Pro	Ser	Phe	Gln	Asp	Tyr	Val	Lys	Asn	
			385					390					395			
tca	gag	aaa	acc	agc	tgc	att	tat	acc	atg	ttt	gct	tct	atc	atc	cca	1309
Ser	Glu	Lys	Thr	Ser	Cys	Ile	Tyr	Thr	Met	Phe	Ala	Ser	Ile	Ile	Pro	
			400					405				410				
ggc	ttg	aaa	tct	gtt	acc	caa	gaa	acc	att	gat	tgg	atc	aag	agt	gaa	1357
Gly	Leu	Lys	Ser	Val	Thr	Gln	Glu	Thr								

465	470	475	
tct aag ttt gaa gga ttg gtt gag gaa aca tgg aag gat ata aac aag			1549
Ser Lys Phe Glu Gly Leu Val Glu Thr Trp Lys Asp Ile Asn Lys			
480	485	490	
gaa ttc ata gcc aca act aat tat aat gtg ggt aga gaa att gcc atc			1597
Glu Phe Ile Ala Thr Thr Asn Tyr Asn Val Gly Arg Glu Ile Ala Ile			
495	500	505	
aca ttc ctc aac tac gct cgg ata tgt gaa gcc agt tac agc aaa act			1645
Thr Phe Leu Asn Tyr Ala Arg Ile Cys Glu Ala Ser Tyr Ser Lys Thr			
510	515	520	525
gac gga gac gct tat tca gat cct aat gtt gcc aag gca aat gtc gtt			1693
Asp Gly Asp Ala Tyr Ser Asp Pro Asn Val Ala Lys Ala Asn Val Val			
530	535	540	
gct ctc ttt gtt gat gcc ata gtc ttt tga tttgcataat caaagaccct			1743
Ala Leu Phe Val Asp Ala Ile Val Phe			
545	550		
ataattataa ttatatgtgt ttaagaaact aataagcttg ctttatgtat agttgtcaat			1803
tgaataataa tgtattaatt agtagagtta agaagttata aagaataaag aggagctggg			1863
agacgtaaac aagaaataat gtgtcaaaat aacttcaact ttttcaagaa taaagaattg			1923
gaagagacca atatatacaa aaaaaaaaaa aaaaaa			1959

&lt;210&gt; 28

&lt;211&gt; 550

&lt;212&gt; PRT

&lt;213&gt; Mentha x piperita

&lt;400&gt; 28

Met	Ala	Thr	Asn	Gly	Val	Val	Ile	Ser	Cys	Leu	Arg	Glu	Val	Arg	Pro
1				5					10					15	
Pro	Met	Thr	Lys	His	Ala	Pro	Ser	Met	Trp	Thr	Asp	Thr	Phe	Ser	Asn
			20					25					30		
Phe	Ser	Leu	Asp	Asp	Lys	Glu	Gln	Gln	Lys	Cys	Ser	Glu	Thr	Ile	Glu
		35				40						45			
Ala	Leu	Lys	Gln	Glu	Ala	Arg	Gly	Met	Leu	Met	Ala	Ala	Thr	Thr	Pro
	50				55					60					
Leu	Gln	Gln	Met	Thr	Leu	Ile	Asp	Thr	Leu	Glu	Arg	Leu	Gly	Leu	Ser
65				70					75					80	
Phe	His	Phe	Glu	Thr	Glu	Ile	Glu	Tyr	Lys	Ile	Glu	Leu	Ile	Asn	Ala
			85					90						95	
Ala	Glu	Asp	Asp	Gly	Phe	Asp	Leu	Phe	Ala	Thr	Ala	Leu	Arg	Phe	Arg
		100					105					110			
Leu	Leu	Arg	Gln	His	Gln	Arg	His	Val	Ser	Cys	Asp	Val	Phe	Asp	Lys
		115				120						125			
Phe	Ile	Asp	Lys	Asp	Gly	Lys	Phe	Glu	Glu	Ser	Leu	Ser	Asn	Asn	Val
	130					135					140				
Glu	Gly	Leu	Leu	Ser	Leu	Tyr	Glu	Ala	Ala	His	Val	Gly	Phe	Arg	Glu
145				150						155				160	
Glu	Arg	Ile	Leu	Gln	Glu	Ala	Val	Asn	Phe	Thr	Arg	His	His	Leu	Glu
			165					170					175		
Gly	Ala	Glu	Leu	Asp	Gln	Ser	Pro	Leu	Leu	Ile	Arg	Glu	Lys	Val	Lys
		180						185					190		

F03230-032660

```
<210> 29
<211> 2196
<212> DNA
<213> Abies grandis

<220>
<221> CDS
<222> (69)...(1949)
<223> myrcene synthase
```



tgccggcacg aggttatctt gagcttcttc catataggcc aacacatatc atatcaaagg	60
gagcaaga atg gct ctg gtt tct atc tca ccg ttg gct tcg aaa tct tgc	110
Met Ala Leu Val Ser Ile Ser Pro Leu Ala Ser Lys Ser Cys	
1 5 10	
ctg cgc aag tcg ttg atc agt tca att cat gaa cat aag cct ccc tat	158
Leu Arg Lys Ser Leu Ile Ser Ser Ile His Glu His Lys Pro Pro Tyr	
15 20 25 30	
aga aca atc cca aat ctt gga atg cgt agg cga ggg aaa tct gtc acg	206
Arg Thr Ile Pro Asn Leu Gly Met Arg Arg Gly Lys Ser Val Thr	
35 40 45	
cct tcc atg agc atc agt ttg gcc acc gct gca cct gat gat ggt gta	254
Pro Ser Met Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val	
50 55 60	
caa aga cgc ata ggt gac tac cat tcc aat atc tgg gac gat gat ttc	302
Gln Arg Arg Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe	
65 70 75	
ata cag tct cta tca acg cct tat ggg gaa ccc tct tac cag gaa cgt	350
Ile Gln Ser Leu Ser Thr Pro Tyr Gly Glu Pro Ser Tyr Gln Glu Arg	
80 85 90	
gct gag aga tta att gtg gag gta aag aag ata ttc aat tca atg tac	398
Ala Glu Arg Leu Ile Val Glu Val Lys Lys Ile Phe Asn Ser Met Tyr	
95 100 105 110	
ctg gat gat gga aga tta atg agt tcc ttt aat gat ctc atg caa cgc	446
Leu Asp Asp Gly Arg Leu Met Ser Ser Phe Asn Asp Leu Met Gln Arg	
115 120 125	
ctt tgg ata gtc gat agc gtt gaa cgt ttg ggg ata gct aga cat ttc	494
Leu Trp Ile Val Asp Ser Val Glu Arg Leu Gly Ile Ala Arg His Phe	
130 135 140	
aag aac gag ata aca tca gct ctg gat tat gtt ttc cgt tac tgg gag	542
Lys Asn Glu Ile Thr Ser Ala Leu Asp Tyr Val Phe Arg Tyr Trp Glu	
145 150 155	
gaa aac ggc att gga tgt ggg aga gac agt att gtt act gat ctc aac	590
Glu Asn Gly Ile Gly Cys Gly Arg Asp Ser Ile Val Thr Asp Leu Asn	
160 165 170	
tca act gcg ttg ggg ttt cga act ctt cga tta cac ggg tac act gta	638
Ser Thr Ala Leu Gly Phe Arg Thr Leu Arg Leu His Gly Tyr Thr Val	
175 180 185 190	
tct cca gag gtt tta aaa gct ttt caa gat caa aat gga cag ttt gta	686
Ser Pro Glu Val Leu Lys Ala Phe Gln Asp Gln Asn Gly Gln Phe Val	
195 200 205	
tgc tcc ccc ggt cag aca gag ggt gag atc aga agc gtt ctt aac tta	734
Cys Ser Pro Gly Gln Thr Glu Gly Glu Ile Arg Ser Val Leu Asn Leu	
210 215 220	

tat Tyr	cgg Arg	gct Ala	tcc Ser	ctc Leu	att Ile	gcc Ala	ttc Phe	cct Pro	ggt Gly	gag Glu	aaa Lys	gtt Val	atg Met	gaa Glu	gaa Glu	782
225230235																
gct Ala	gaa Glu	atc Ile	ttc Phe	tcc Ser	aca Thr	aga Arg	tat Tyr	ttg Leu	aaa Lys	gaa Glu	gct Ala	cta Leu	caa Gln	aag Lys	att Ile	830
240245250																
cca Pro	gtc Val	tcc Ser	gct Ala	ctt Leu	tca Ser	caa Gln	gag Glu	ata Ile	aag Lys	ttt Phe	gtt Val	atg Met	gaa Glu	tat Tyr	ggc Gly	878
255260265270																
tgg Trp	cac His	aca Thr	aat Asn	ttg Leu	cca Pro	aga Arg	ttg Leu	gaa Glu	gca Ala	aga Arg	aat Asn	tac Tyr	ata Ile	gac Asp	aca Thr	926
275280285																
ctt Leu	gag Glu	aaa Lys	gac Asp	acc Thr	agt Ser	gca Ala	tgg Trp	ctc Leu	aat Asn	aaa Lys	aat Asn	gct Ala	ggg Gly	aag Lys	aag Lys	974
290295300																
ctt Leu	tta Leu	gaa Glu	ctt Leu	gca Ala	aaa Lys	ttg Leu	gag Glu	ttc Phe	aat Asn	ata Ile	ttt Phe	aac Asn	tcc Ser	tta Leu	caa Gln	1022
305310315																
caa Gln	aag Lys	gaa Glu	tta Leu	caa Gln	tat Tyr	ctt Leu	ttg Leu	aga Arg	tgg Trp	tgg Trp	aaa Lys	gag Glu	tcg Ser	gat Asp	ttg Leu	1070
320325330																
cct Pro	aaa Lys	ttg Leu	aca Thr	ttt Phe	gct Ala	cgg Arg	cat His	cgt Arg	cat His	gtg Val	gaa Glu	ttc Phe	tac Tyr	act Thr	ttg Leu	1118
335340345350																
gcc Ala	tct Ser	tgt Cys	att Ile	gcc Ala	att Ile	gac Asp	cca Pro	aaa Lys	cat His	tct Ser	gca Ala	ttc Phe	aga Arg	cta Leu	ggc Gly	1166
355360365																
ttc Phe	gcc Ala	aaa Lys	atg Met	tgt Cys	cat His	ctt Leu	gtc Val	aca Thr	gtt Val	ttg Leu	gac Asp	gat Asp	att Ile	tac Tyr	gac Asp	1214
370375380																
act Thr	ttt Phe	gga Gly	acg Thr	att Ile	gac Asp	gag Glu	ctt Leu	gaa Glu	ctc Leu	ttc Phe	aca Thr	tct Ser	gca Ala	att Ile	aag Lys	1262
385390395																
aga Arg	tgg Trp	aat Asn	tca Ser	tca Ser	gag Glu	ata Ile	gaa Glu	cac His	ctt Leu	cca Pro	gaa Glu	tat Tyr	atg Met	aaa Lys	tgt Cys	1310
400405410																
gtg Val	tac Tyr	atg Met	gtc Val	gtg Val	ttt Phe	gaa Glu	act Thr	gta Val	aat Asn	gaa Glu	ctg Leu	aca Thr	cga Arg	gag Glu	gcg Ala	1358
415420425430																
gag Glu	aag Lys	act Thr	caa Gln	ggg Gly	aga Arg	aac Asn	act Thr	ctc Leu	aac Asn	tat Tyr	gtt Val	cga Arg	aag Lys	gct Ala	tgg Trp	1406
435440445																

```
<210> 30
<211> 627
<212> PRT
<213> Abies grandis
```

&lt;400&gt; 30

Met	Ala	Leu	Val	Ser	Ile	Ser	Pro	Leu	Ala	Ser	Lys	Ser	Cys	Leu	Arg
1				5					10					15	
Lys	Ser	Leu	Ile	Ser	Ser	Ile	His	Glu	His	Lys	Pro	Pro	Tyr	Arg	Thr
			20					25					30		
Ile	Pro	Asn	Leu	Gly	Met	Arg	Arg	Arg	Gly	Lys	Ser	Val	Thr	Pro	Ser
		35					40					45			
Met	Ser	Ile	Ser	Leu	Ala	Thr	Ala	Ala	Pro	Asp	Asp	Gly	Val	Gln	Arg
	50					55				60					
Arg	Ile	Gly	Asp	Tyr	His	Ser	Asn	Ile	Trp	Asp	Asp	Asp	Phe	Ile	Gln
65					70				75					80	
Ser	Leu	Ser	Thr	Pro	Tyr	Gly	Glu	Pro	Ser	Tyr	Gln	Glu	Arg	Ala	Glu
				85				90						95	
Arg	Leu	Ile	Val	Glu	Val	Lys	Lys	Ile	Phe	Asn	Ser	Met	Tyr	Leu	Asp
			100					105					110		
Asp	Gly	Arg	Leu	Met	Ser	Ser	Phe	Asn	Asp	Leu	Met	Gln	Arg	Leu	Trp
		115					120					125			
Ile	Val	Asp	Ser	Val	Glu	Arg	Leu	Gly	Ile	Ala	Arg	His	Phe	Lys	Asn
	130					135					140				
Glu	Ile	Thr	Ser	Ala	Leu	Asp	Tyr	Val	Phe	Arg	Tyr	Trp	Glu	Glu	Asn
145					150				155						160
Gly	Ile	Gly	Cys	Gly	Arg	Asp	Ser	Ile	Val	Thr	Asp	Leu	Asn	Ser	Thr
				165				170						175	
Ala	Leu	Gly	Phe	Arg	Thr	Leu	Arg	Leu	His	Gly	Tyr	Thr	Val	Ser	Pro
			180					185					190		
Glu	Val	Leu	Lys	Ala	Phe	Gln	Asp	Gln	Asn	Gly	Gln	Phe	Val	Cys	Ser
		195					200					205			
Pro	Gly	Gln	Thr	Glu	Gly	Glu	Ile	Arg	Ser	Val	Leu	Asn	Leu	Tyr	Arg
	210					215					220				
Ala	Ser	Leu	Ile	Ala	Phe	Pro	Gly	Glu	Lys	Val	Met	Glu	Glu	Ala	Glu
225					230				235					240	
Ile	Phe	Ser	Thr	Arg	Tyr	Leu	Lys	Glu	Ala	Leu	Gln	Lys	Ile	Pro	Val
				245				250						255	
Ser	Ala	Leu	Ser	Gln	Glu	Ile	Lys	Phe	Val	Met	Glu	Tyr	Gly	Trp	His
		260						265					270		
Thr	Asn	Leu	Pro	Arg	Leu	Glu	Ala	Arg	Asn	Tyr	Ile	Asp	Thr	Leu	Glu
		275					280						285		
Lys	Asp	Thr	Ser	Ala	Trp	Leu	Asn	Lys	Asn	Ala	Gly	Lys	Lys	Leu	Leu
	290					295					300				
Glu	Leu	Ala	Lys	Leu	Glu	Phe	Asn	Ile	Phe	Asn	Ser	Leu	Gln	Gln	Lys
305					310				315						320
Glu	Leu	Gln	Tyr	Leu	Leu	Arg	Trp	Trp	Lys	Glu	Ser	Asp	Leu	Pro	Lys
				325					330					335	
Leu	Thr	Phe	Ala	Arg	His	Arg	His	Val	Glu	Phe	Tyr	Thr	Leu	Ala	Ser
			340					345					350		
Cys	Ile	Ala	Ile	Asp	Pro	Lys	His	Ser	Ala	Phe	Arg	Leu	Gly	Phe	Ala
		355					360					365			
Lys	Met	Cys	His	Leu	Val	Thr	Val	Leu	Asp	Asp	Ile	Tyr	Asp	Thr	Phe
	370					375					380				
Gly	Thr	Ile	Asp	Glu	Leu	Glu	Leu	Phe	Thr	Ser	Ala	Ile	Lys	Arg	Trp
385					390				395					400	
Asn	Ser	Ser	Glu	Ile	Glu	His	Leu	Pro	Glu	Tyr	Met	Lys	Cys	Val	Tyr
			405					410						415	
Met	Val	Val	Phe	Glu	Thr	Val	Asn	Glu	Leu	Thr	Arg	Glu	Ala	Glu	Lys
			420					425					430		
Thr	Gln	Gly	Arg	Asn	Thr	Leu	Asn	Tyr	Val	Arg	Lys	Ala	Trp	Glu	Ala

T02290" 0222500

435 440 445  
 Tyr Phe Asp Ser Tyr Met Glu Glu Ala Lys Trp Ile Ser Asn Gly Tyr  
 450 455 460  
 Leu Pro Met Phe Glu Glu Tyr His Glu Asn Gly Lys Val Ser Ser Ala  
 465 470 475 480  
 Tyr Arg Val Ala Thr Leu Gln Pro Ile Leu Thr Leu Asn Ala Trp Leu  
 485 490 495  
 Pro Asp Tyr Ile Leu Lys Gly Ile Asp Phe Pro Ser Arg Phe Asn Asp  
 500 505 510  
 Leu Ala Ser Ser Phe Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys  
 515 520 525  
 Ala Asp Arg Asp Arg Gly Glu Glu Ala Ser Cys Ile Ser Cys Tyr Met  
 530 535 540  
 Lys Asp Asn Pro Gly Ser Thr Glu Glu Asp Ala Leu Asn His Ile Asn  
 545 550 555 560  
 Ala Met Val Asn Asp Ile Ile Lys Glu Leu Asn Trp Glu Leu Leu Arg  
 565 570 575  
 Ser Asn Asp Asn Ile Pro Met Leu Ala Lys Lys His Ala Phe Asp Ile  
 580 585 590  
 Thr Arg Ala Leu His His Leu Tyr Ile Tyr Arg Asp Gly Phe Ser Val  
 595 600 605  
 Ala Asn Lys Glu Thr Lys Lys Leu Val Met Glu Thr Leu Leu Glu Ser  
 610 615 620  
 Met Leu Phe  
 625

<210> 31  
 <211> 1944  
 <212> DNA  
 <213> Solanum tuberosum  
 <220>  
 <221> CDS  
 <222> (57)...(1724)  
 <223> vetispiradiene synthase

<400> 31  
 gaaagaaaga aaattctctc tgttttttcc acaagcaaag agtacacaca ctagaa atg 59  
 Met  
 1  
 acc cca gct gct gta gta atg agt aac tac gga gag gag gag att gtt 107  
 Thr Pro Ala Ala Val Val Met Ser Asn Tyr Gly Glu Glu Glu Ile Val  
 5 10 15  
 cgc ccc ata gct gac ttc tct cca agt ctt tgg ggt gat cgt ttt cat 155  
 Arg Pro Ile Ala Asp Phe Ser Pro Ser Leu Trp Gly Asp Arg Phe His  
 20 25 30  
 tca ttc tcc ctc gac aat cag att gct gga aaa tat gct caa gag atc 203  
 Ser Phe Ser Ser Leu Asp Asn Gln Ile Ala Gly Lys Tyr Ala Gln Glu Ile  
 35 40 45  
 gaa act ttg aag gaa caa tca aga att ata tta tct gca tct tct cga 251  
 Glu Thr Leu Lys Glu Gln Ser Arg Ile Ile Leu Ser Ala Ser Ser Arg  
 50 55 60 65

T.D3290-02EE666

aga aca ttg gct gag aaa ttg gat ctg ata gac att gtt gag cgc ctt	299
Arg Thr Leu Ala Glu Lys Leu Asp Leu Ile Asp Ile Val Glu Arg Leu	
70 75 80	
ggc att gct tat cat ttt gaa aaa caa ata gat gat atg ttg gat caa	347
Gly Ile Ala Tyr His Phe Glu Lys Gln Ile Asp Asp Met Leu Asp Gln	
85 90 95	
ttt tac aaa gca gat cct aac ttt gag gct cac gag tac aat gat tta	395
Phe Tyr Lys Ala Asp Pro Asn Phe Glu Ala His Glu Tyr Asn Asp Leu	
100 105 110	
caa act tta tcc gtt caa ttt cga cta ttg aga caa cat ggt tac aat	443
Gln Thr Leu Ser Val Gln Phe Arg Leu Leu Arg Gln His Gly Tyr Asn	
115 120 125	
atc tcc cca aaa ctt ttt att aga ttc caa gat gca aaa ggc aaa ttt	491
Ile Ser Pro Lys Leu Phe Ile Arg Phe Gln Asp Ala Lys Gly Lys Phe	
130 135 140 145	
aaa gaa tct ctt tgt aac gac atc aag ggt ctt ttg aac tta tac gaa	539
Lys Glu Ser Leu Cys Asn Asp Ile Lys Gly Leu Leu Asn Leu Tyr Glu	
150 155 160	
gcc tcg cat gta agg act cat gga gaa gat att ttg gaa gag gca ctt	587
Ala Ser His Val Arg Thr His Gly Glu Asp Ile Leu Glu Glu Ala Leu	
165 170 175	
gct ttc tct act gct cat ctt gaa tct gca gct cca cat ttg aag tca	635
Ala Phe Ser Thr Ala His Leu Glu Ser Ala Ala Pro His Leu Lys Ser	
180 185 190	
cct ctg agt aag caa gtg aca cat gcc ctt gag caa tct ctc cat aag	683
Pro Leu Ser Lys Gln Val Thr His Ala Leu Glu Gln Ser Leu His Lys	
195 200 205	
agc att cca aga gtt gag aca cgc tac ttc atc tct atc tac gaa gag	731
Ser Ile Pro Arg Val Glu Thr Arg Tyr Phe Ile Ser Ile Tyr Glu Glu	
210 215 220 225	
gag gaa cag aag aat gat gtg ttg ctt caa ttt gca aaa ctg gac ttc	779
Glu Glu Gln Lys Asn Asp Val Leu Leu Gln Phe Ala Lys Leu Asp Phe	
230 235 240	
aac tta ctt cag atg ttg cac aaa caa gaa ctt agt gaa gta tca agg	827
Asn Leu Leu Gln Met Leu His Lys Gln Glu Leu Ser Glu Val Ser Arg	
245 250 255	
tgg tgg aaa gat ttg gat ttt gtg aca aca ctt cca tat gct agg gat	875
Trp Trp Lys Asp Leu Asp Phe Val Thr Thr Leu Pro Tyr Ala Arg Asp	
260 265 270	
aga gca gtg gaa tgc tac ttt tgg acg atg ggg gtg tat gct gaa cct	923
Arg Ala Val Glu Cys Tyr Phe Trp Thr Met Gly Val Tyr Ala Glu Pro	
275 280 285	
caa tac tct cag gct cgt gtc atg ctt gct aag act ata gca atg att	971

Gln	Tyr	Ser	Gln	Ala	Arg	Val	Met	Leu	Ala	Lys	Thr	Ile	Ala	Met	Ile	
290					295					300					305	
tct	ata	gta	gat	gac	aca	ttc	gat	gct	tat	ggc	att	gtc	aaa	gaa	ctt	1019
Ser	Ile	Val	Asp	Asp	Thr	Phe	Asp	Ala	Tyr	Gly	Ile	Val	Lys	Glu	Leu	
				310					315					320		
gag	atc	tac	acc	gat	gcc	ata	cag	agg	tgg	gat	att	agc	caa	att	gat	1067
Glu	Ile	Tyr	Thr	Asp	Ala	Ile	Gln	Arg	Trp	Asp	Ile	Ser	Gln	Ile	Asp	
			325					330					335			
cgg	ctc	cct	gat	tac	atg	aaa	atc	agt	tac	aaa	gca	ctt	tta	gat	ctc	1115
Arg	Leu	Pro	Asp	Tyr	Met	Lys	Ile	Ser	Tyr	Lys	Ala	Leu	Leu	Asp	Leu	
		340					345					350				
tac	aat	gat	tat	gaa	atg	gag	ttg	tcc	aag	gat	ggt	aga	tct	gat	gtt	1163
Tyr	Asn	Asp	Tyr	Glu	Met	Glu	Leu	Ser	Lys	Asp	Gly	Arg	Ser	Asp	Val	
	355					360					365					
gtt	cac	tac	gcg	aaa	gaa	aga	atg	aaa	gaa	atc	gtg	aga	aac	tat	ttt	1211
Val	His	Tyr	Ala	Lys	Glu	Arg	Met	Lys	Glu	Ile	Val	Arg	Asn	Tyr	Phe	
370				375						380					385	
gtg	gaa	gca	aaa	tgg	ttc	att	gaa	gga	tat	atg	ccg	cca	gtc	tct	gag	1259
Val	Glu	Ala	Lys	Trp	Phe	Ile	Glu	Gly	Tyr	Met	Pro	Pro	Val	Ser	Glu	
				390					395					400		
tat	ctt	agc	aat	gca	tta	gct	acc	agc	act	tat	tac	ttg	ctt	acg	act	1307
Tyr	Leu	Ser	Asn	Ala	Leu	Ala	Thr	Ser	Thr	Tyr	Tyr	Leu	Leu	Thr	Thr	
			405					410					415			
aca	tct	tat	ttg	ggc	atg	aag	tct	gct	aac	aag	caa	gat	ttt	gaa	tgg	1355
Thr	Ser	Tyr	Leu	Gly	Met	Lys	Ser	Ala	Asn	Lys	Gln	Asp	Phe	Glu	Trp	
		420					425					430				
ttg	gcc	aag	aac	cct	aaa	att	ctt	gag	gct	aat	gtg	acg	tta	tgc	cga	1403
Leu	Ala	Lys	Asn	Pro	Lys	Ile	Leu	Glu	Ala	Asn	Val	Thr	Leu	Cys	Arg	
	435					440					445					
gtc	ata	gat	gac	ata	gcc	acc	tat	gag	gtt	gag	aag	ggt	aga	ggt	cag	1451
Val	Ile	Asp	Asp	Ile	Ala	Thr	Tyr	Glu	Val	Glu	Lys	Gly	Arg	Gly	Gln	
450				455					460					465		
att	gcc	act	gga	att	gaa	tgt	tac	atg	aga	gat	tat	ggt	gta	tcc	aca	1499
Ile	Ala	Thr	Gly	Ile	Glu	Cys	Tyr	Met	Arg	Asp	Tyr	Gly	Val	Ser	Thr	
			470					475					480			
gaa	aag	gcc	atg	gaa	aaa	ttc	caa	gaa	atg	gct	gag	aca	gca	tgg	aag	1547
Glu	Lys	Ala	Met	Glu	Lys	Phe	Gln	Glu	Met	Ala	Glu	Thr	Ala	Trp	Lys	
			485					490					495			
gat	gta	aat	gaa	gga	atc	ctt	cga	cca	act	ccc	gtc	tct	aca	gag	att	1595
Asp	Val	Asn	Glu	Gly	Ile	Leu	Arg	Pro	Thr	Pro	Val	Ser	Thr	Glu	Ile	
		500					505					510				
ctc	act	cgc	att	ctc	aat	ctt	gct	cgc	att	atc	gat	gtt	act	tat	aag	1643
Leu	Thr	Arg	Ile	Leu	Asn	Leu	Ala	Arg	Ile	Ile	Asp	Val	Thr	Tyr	Lys	

T000290"02236880

515

520

525

cac aat caa gat gga tac act cat ccg gaa aaa gta cta aaa cct cat 1691  
 His Asn Gln Asp Gly Tyr Thr His Pro Glu Lys Val Leu Lys Pro His  
 530 535 540 545

att att gcg ttg ttg gtg gac tct att gaa att taa atcatcgatt 1737  
 Ile Ile Ala Leu Leu Val Asp Ser Ile Glu Ile  
 550 555

gttttgtaca tctgggagca cttgcttccc atcccctaaa attataagta tttgattgat 1797  
 gccttggttg tatctatgct gctaggcgct agctaagata ggagttgctg gagatacatg 1857  
 ttatagtgc gtgcagttaa ttccttaatt tttttttgta tcattattga catttttaaat 1917  
 atatatatat atatcactgc tttttat 1944

&lt;210&gt; 32

&lt;211&gt; 556

&lt;212&gt; PRT

&lt;213&gt; Solanum tuberosum

&lt;400&gt; 32

Met Thr Pro Ala Ala Val Val Met Ser Asn Tyr Gly Glu Glu Glu Ile  
 1 5 10 15  
 Val Arg Pro Ile Ala Asp Phe Ser Pro Ser Leu Trp Gly Asp Arg Phe  
 20 25 30  
 His Ser Phe Ser Leu Asp Asn Gln Ile Ala Gly Lys Tyr Ala Gln Glu  
 35 40 45  
 Ile Glu Thr Leu Lys Glu Gln Ser Arg Ile Ile Leu Ser Ala Ser Ser  
 50 55 60  
 Arg Arg Thr Leu Ala Glu Lys Leu Asp Leu Ile Asp Ile Val Glu Arg  
 65 70 75 80  
 Leu Gly Ile Ala Tyr His Phe Glu Lys Gln Ile Asp Asp Met Leu Asp  
 85 90 95  
 Gln Phe Tyr Lys Ala Asp Pro Asn Phe Glu Ala His Glu Tyr Asn Asp  
 100 105 110  
 Leu Gln Thr Leu Ser Val Gln Phe Arg Leu Leu Arg Gln His Gly Tyr  
 115 120 125  
 Asn Ile Ser Pro Lys Leu Phe Ile Arg Phe Gln Asp Ala Lys Gly Lys  
 130 135 140  
 Phe Lys Glu Ser Leu Cys Asn Asp Ile Lys Gly Leu Leu Asn Leu Tyr  
 145 150 155 160  
 Glu Ala Ser His Val Arg Thr His Gly Glu Asp Ile Leu Glu Glu Ala  
 165 170 175  
 Leu Ala Phe Ser Thr Ala His Leu Glu Ser Ala Ala Pro His Leu Lys  
 180 185 190  
 Ser Pro Leu Ser Lys Gln Val Thr His Ala Leu Glu Gln Ser Leu His  
 195 200 205  
 Lys Ser Ile Pro Arg Val Glu Thr Arg Tyr Phe Ile Ser Ile Tyr Glu  
 210 215 220  
 Glu Glu Glu Gln Lys Asn Asp Val Leu Leu Gln Phe Ala Lys Leu Asp  
 225 230 235 240  
 Phe Asn Leu Leu Gln Met Leu His Lys Gln Glu Leu Ser Glu Val Ser  
 245 250 255  
 Arg Trp Trp Lys Asp Leu Asp Phe Val Thr Thr Leu Pro Tyr Ala Arg  
 260 265 270  
 Asp Arg Ala Val Glu Cys Tyr Phe Trp Thr Met Gly Val Tyr Ala Glu  
 275 280 285

F002299-0226659



Pro Gln Tyr Ser Gln Ala Arg Val Met Leu Ala Lys Thr Ile Ala Met  
 290 295 300  
 Ile Ser Ile Val Asp Asp Thr Phe Asp Ala Tyr Gly Ile Val Lys Glu  
 305 310 315 320  
 Leu Glu Ile Tyr Thr Asp Ala Ile Gln Arg Trp Asp Ile Ser Gln Ile  
 325 330 335  
 Asp Arg Leu Pro Asp Tyr Met Lys Ile Ser Tyr Lys Ala Leu Leu Asp  
 340 345 350  
 Leu Tyr Asn Asp Tyr Glu Met Glu Leu Ser Lys Asp Gly Arg Ser Asp  
 355 360 365  
 Val Val His Tyr Ala Lys Glu Arg Met Lys Glu Ile Val Arg Asn Tyr  
 370 375 380  
 Phe Val Glu Ala Lys Trp Phe Ile Glu Gly Tyr Met Pro Pro Val Ser  
 385 390 395 400  
 Glu Tyr Leu Ser Asn Ala Leu Ala Thr Ser Thr Tyr Tyr Leu Leu Thr  
 405 410 415  
 Thr Thr Ser Tyr Leu Gly Met Lys Ser Ala Asn Lys Gln Asp Phe Glu  
 420 425 430  
 Trp Leu Ala Lys Asn Pro Lys Ile Leu Glu Ala Asn Val Thr Leu Cys  
 435 440 445  
 Arg Val Ile Asp Asp Ile Ala Thr Tyr Glu Val Glu Lys Gly Arg Gly  
 450 455 460  
 Gln Ile Ala Thr Gly Ile Glu Cys Tyr Met Arg Asp Tyr Gly Val Ser  
 465 470 475 480  
 Thr Glu Lys Ala Met Glu Lys Phe Gln Glu Met Ala Glu Thr Ala Trp  
 485 490 495  
 Lys Asp Val Asn Glu Gly Ile Leu Arg Pro Thr Pro Val Ser Thr Glu  
 500 505 510  
 Ile Leu Thr Arg Ile Leu Asn Leu Ala Arg Ile Ile Asp Val Thr Tyr  
 515 520 525  
 Lys His Asn Gln Asp Gly Tyr Thr His Pro Glu Lys Val Leu Lys Pro  
 530 535 540  
 His Ile Ile Ala Leu Leu Val Asp Ser Ile Glu Ile  
 545 550 555

<210> 33  
 <211> 3950  
 <212> DNA  
 <213> Gossypium arboreum

<220>  
 <221> CDS  
 <222> (1457)...(1579)  
 <223> cadinene synthase

<221> CDS  
 <222> (1670)...(1939)

<221> CDS  
 <222> (2092)...(2466)

<221> CDS  
 <222> (2559)...(2774)

<221> CDS  
 <222> (2963)...(3103)

agt tat cat ttt gag aaa gag att gaa gat gaa cta gag aat att tac 1846

Ser Tyr His Phe Glu Lys Glu Ile Glu Asp Glu Leu Glu Asn Ile Tyr  
 85 90 95 100  
 cgt gac acc aac aac aat gat gcg gac acc gat ctc tac act aca gct 1894  
 Arg Asp Thr Asn Asn Asn Asp Ala Asp Thr Asp Leu Tyr Thr Thr Ala  
 105 110 115  
 ctt cga ttc cgg tta ctt aga gag cat ggc ttc gat att tct tgt 1939  
 Leu Arg Phe Arg Leu Leu Arg Glu His Gly Phe Asp Ile Ser Cys  
 120 125 130  
 ggtaattaag tcttaaactt tcataactct tcttatccat ttatcaatta atattatcaa 1999  
 actttacatt aataatcatc tgtacaatac ttcaatatat atatatttat tgatgaaact 2059  
 aatgtttgat gatgattttg ggtgcttgac ca gat gca ttc aac aag ttc aaa 2112  
 Asp Ala Phe Asn Lys Phe Lys  
 135  
 gat gag gca ggg aac ttc aag gca tca ttg aca agt gat gtg caa ggg 2160  
 Asp Glu Ala Gly Asn Phe Lys Ala Ser Leu Thr Ser Asp Val Gln Gly  
 140 145 150  
 ttg ttg gaa ctt tat gaa gct tcc tat atg agg gtc cat ggg gaa gat 2208  
 Leu Leu Glu Leu Tyr Glu Ala Ser Tyr Met Arg Val His Gly Glu Asp  
 155 160 165 170  
 ata ctt gat gaa gcc att tct ttc acc act gct caa ctt aca ctt gct 2256  
 Ile Leu Asp Glu Ala Ile Ser Phe Thr Thr Ala Gln Leu Thr Leu Ala  
 175 180 185  
 cta cca act tta cac cat cct tta tcg gaa cag gtc ggc cat gcc tta 2304  
 Leu Pro Thr Leu His His Pro Leu Ser Glu Gln Val Gly His Ala Leu  
 190 195 200  
 aag cag tct atc cga agg ggc ttg cca agg gtt gag gcc cgg aat ttc 2352  
 Lys Gln Ser Ile Arg Arg Gly Leu Pro Arg Val Glu Ala Arg Asn Phe  
 205 210 215  
 att tcg ata tac caa gat tta gaa tcc cat aac aaa tcg ttg ctt caa 2400  
 Ile Ser Ile Tyr Gln Asp Leu Glu Ser His Asn Lys Ser Leu Leu Gln  
 220 225 230  
 ttt gca aag att gat ttc aac ttg ttg cag ctt ttg cat agg aaa gag 2448  
 Phe Ala Lys Ile Asp Phe Asn Leu Leu Gln Leu Leu His Arg Lys Glu  
 235 240 245 250  
 cta agt gag atc tgc agg taagtgtttg gagatcttta aagctatgaa 2496  
 Leu Ser Glu Ile Cys Arg  
 255  
 gtctaatact atttcaattg atcacacgac tgttgctgac attttatgat gcttttttta 2556  
 gg tgg tgg aaa gat tta gac ttt aca aga aaa cta cca ttt gca aga 2603  
 Trp Trp Lys Asp Leu Asp Phe Thr Arg Lys Leu Pro Phe Ala Arg  
 260 265 270  
 gat aga gtg gtt gaa ggc tat ttt tgg ata atg gga gtt tac ttt gaa 2651  
 Asp Arg Val Val Glu Gly Tyr Phe Trp Ile Met Gly Val Tyr Phe Glu  
 275 280 285

T02290" 02222222

ccc caa tac tct ctt ggt aga aag atg ttg aca aaa gtc ata gca atg 2699  
Pro Gln Tyr Ser Leu Gly Arg Lys Met Leu Thr Lys Val Ile Ala Met  
290 295 300

gct tcc att gtt gat gat act tat gat tca tat gca acc tat gat gaa 2747  
Ala Ser Ile Val Asp Asp Thr Tyr Asp Ser Tyr Ala Thr Tyr Asp Glu  
305 310 315

ctc att ccc tat aca aat gca att gaa ggtgagattt tttttccttt 2794  
Leu Ile Pro Tyr Thr Asn Ala Ile Glu  
320 325

cctccaaaaa aaaaaaaagt ttttgagatc ccccaagaat aggggaaaaat atatgttttt 2854  
aaacgttagg atattcactc caacttgacg ttgctcatat tttaatggtg atagtatgaa 2914  
ctaaccaggc taagtttttag attcaaatta accctgaaat tgtgtttt agg tgg gat 2971  
Arg Trp Asp  
330

att aaa tgc atg aac caa ctc ccg aat tac atg aaa ata agc tac aag 3019  
Ile Lys Cys Met Asn Gln Leu Pro Asn Tyr Met Lys Ile Ser Tyr Lys  
335 340 345

gca cta tta gat gtt tat gaa gaa atg gaa cag ctg ttg gca aat caa 3067  
Ala Leu Leu Asp Val Tyr Glu Glu Met Glu Gln Leu Leu Ala Asn Gln  
350 355 360

ggg aga cag tac cga gtt gag tat gcg aaa aag gcg gtatgtaatg 3113  
Gly Arg Gln Tyr Arg Val Glu Tyr Ala Lys Lys Ala  
365 370 375

atacaatagt atgatatgct ttaatcataa acgtataaaa tttgaaaatt acattagcaa 3173  
tttgcttact tttttatgcc ttttaatcctc ag atg ata cgt ctt gtt caa gct 3226  
Met Ile Arg Leu Val Gln Ala  
380

tac ctt ttg gag gcc aaa tgg act cat caa aat tat aaa cca acc ttt 3274  
Tyr Leu Leu Glu Ala Lys Trp Thr His Gln Asn Tyr Lys Pro Thr Phe  
385 390 395

gag gaa ttt aga gat aat gca ttg cca acc tct ggc tat gcc atg ctt 3322  
Glu Glu Phe Arg Asp Asn Ala Leu Pro Thr Ser Gly Tyr Ala Met Leu  
400 405 410

gct ata acg gcg ttt gtc ggc atg ggc gaa gtt ata acc cct gag acc 3370  
Ala Ile Thr Ala Phe Val Gly Met Gly Glu Val Ile Thr Pro Glu Thr  
415 420 425 430

ttc aaa tgg gcc gcc agt gac ccc aag atc att aag gct tcc acc att 3418  
Phe Lys Trp Ala Ala Ser Asp Pro Lys Ile Ile Lys Ala Ser Thr Ile  
435 440 445

att tgc agg ttc atg gac gat att gct gaa cat aag gtatactata 3464  
Ile Cys Arg Phe Met Asp Asp Ile Ala Glu His Lys  
450 455

tattcatatt caagaattct aaaaaatcgat tatggatatat atatgcactt aaatctatat 3524

T08090" 02020000

```

<210> 34
<211> 41
<212> PRT
<213> Gossypium arboreum

<400> 34
Met Ala Ser Gln Ala Ser Gln Val Leu Ala Ser Pro His Pro Ala Ile
 1          5          10          15
Ser Ser Glu Asn Arg Pro Lys Ala Asp Phe His Pro Gly Ile Trp Gly
 20          25          30
Asp Met Phe Ile Ile Cys Pro Asp Thr
 35          40

<210> 35
<211> 90
<212> PRT
<213> Gossypium arboreum

<400> 35
Asp Ile Asp Ala Ala Thr Glu Leu Gln Tyr Glu Glu Leu Lys Ala Gln
 1          5          10          15
Val Arg Lys Met Ile Met Glu Pro Val Asp Asp Ser Asn Gln Lys Leu
 20          25          30
Pro Phe Ile Asp Ala Val Gln Arg Leu Gly Val Ser Tyr His Phe Glu
 35          40          45
Lys Glu Ile Glu Asp Glu Leu Glu Asn Ile Tyr Arg Asp Thr Asn Asn

```

50                      55                      60  
 Asn Asp Ala Asp Thr Asp Leu Tyr Thr Thr Ala Leu Arg Phe Arg Leu  
 65                      70                      75                      80  
 Leu Arg Glu His Gly Phe Asp Ile Ser Cys  
                     85                      90

<210> 36  
 <211> 125  
 <212> PRT  
 <213> Gossypium arboreum

<400> 36  
 Asp Ala Phe Asn Lys Phe Lys Asp Glu Ala Gly Asn Phe Lys Ala Ser  
 1                      5                      10                      15  
 Leu Thr Ser Asp Val Gln Gly Leu Leu Glu Leu Tyr Glu Ala Ser Tyr  
                     20                      25                      30  
 Met Arg Val His Gly Glu Asp Ile Leu Asp Glu Ala Ile Ser Phe Thr  
                     35                      40                      45  
 Thr Ala Gln Leu Thr Leu Ala Leu Pro Thr Leu His His Pro Leu Ser  
                     50                      55                      60  
 Glu Gln Val Gly His Ala Leu Lys Gln Ser Ile Arg Arg Gly Leu Pro  
 65                      70                      75                      80  
 Arg Val Glu Ala Arg Asn Phe Ile Ser Ile Tyr Gln Asp Leu Glu Ser  
                     85                      90                      95  
 His Asn Lys Ser Leu Leu Gln Phe Ala Lys Ile Asp Phe Asn Leu Leu  
                     100                      105                      110  
 Gln Leu Leu His Arg Lys Glu Leu Ser Glu Ile Cys Arg  
                     115                      120                      125

<210> 37  
 <211> 72  
 <212> PRT  
 <213> Gossypium arboreum

<400> 37  
 Trp Trp Lys Asp Leu Asp Phe Thr Arg Lys Leu Pro Phe Ala Arg Asp  
 1                      5                      10                      15  
 Arg Val Val Glu Gly Tyr Phe Trp Ile Met Gly Val Tyr Phe Glu Pro  
                     20                      25                      30  
 Gln Tyr Ser Leu Gly Arg Lys Met Leu Thr Lys Val Ile Ala Met Ala  
                     35                      40                      45  
 Ser Ile Val Asp Asp Thr Tyr Asp Ser Tyr Ala Thr Tyr Asp Glu Leu  
                     50                      55                      60  
 Ile Pro Tyr Thr Asn Ala Ile Glu  
 65                      70

<210> 38  
 <211> 47  
 <212> PRT  
 <213> Gossypium arboreum

<400> 38  
 Arg Trp Asp Ile Lys Cys Met Asn Gln Leu Pro Asn Tyr Met Lys Ile  
 1                      5                      10                      15  
 Ser Tyr Lys Ala Leu Leu Asp Val Tyr Glu Glu Met Glu Gln Leu Leu  
                     20                      25                      30  
 Ala Asn Gln Gly Arg Gln Tyr Arg Val Glu Tyr Ala Lys Lys Ala

F08290" 03226660

45

```
<400> 39
Met Ile Arg Leu Val Gln Ala Tyr Leu Leu Glu Ala Lys Trp Thr His
  1             5             10             15
Gln Asn Tyr Lys Pro Thr Phe Glu Glu Phe Arg Asp Asn Ala Leu Pro
  20             25             30
Thr Ser Gly Tyr Ala Met Leu Ala Ile Thr Ala Phe Val Gly Met Gly
  35             40             45
Glu Val Ile Thr Pro Glu Thr Phe Lys Trp Ala Ala Ser Asp Pro Lys
  50             55             60
Ile Ile Lys Ala Ser Thr Ile Ile Cys Arg Phe Met Asp Asp Ile Ala
  65             70             75             80
Glu His Lys
```

```

<400> 40
Phe Asn His Arg Arg Glu Asp Asp Cys Ser Ala Ile Glu Cys Tyr Met
 1          5          10          15
Lys Gln Tyr Gly Val Thr Ala Gln Glu Ala Tyr Asn Glu Phe Asn Lys
          20          25          30
His Ile Glu Ser Ser Trp Lys Asp Val Asn Glu Glu Phe Leu Lys Pro
          35          40          45
Thr Glu Met Pro Thr Pro Val Leu Cys Arg Ser Leu Asn Leu Ala Arg
          50          55          60
Val Met Asp Val Leu Tyr Arg Glu Gly Asp Gly Tyr Thr His Val Gly
65          70          75          80
Lys Ala Ala Lys Gly Ile Thr Ser Leu Leu Ile Asp Pro Ile Gln
          85          90          95
Ile

```

```
<220>
<221> CDS
<222> (67)...(1869)
<223> casbene synthase
```

```

<400> 41
actcagcagc cgccctctcct accccaatta gcacagaaga tttggtgggt cctctccttg      60
tgaaac atg gca ttg cca tca gct gct atg caa tcc aac cct gaa aag      108
      Met Ala Leu Pro Ser Ala Ala Met Gln Ser Asn Pro Glu Lys
            1             5             10

```

ctt aac tta ttt cac aga ttg tca agc tta ccc acc act agc ttg gaa	156
Leu Asn Leu Phe His Arg Leu Ser Ser Leu Pro Thr Thr Ser Leu Glu	
15 20 25 30	
tat ggc aat aat cgc ttc cct ttc ttt tcc tca tct gcc aag tca cac	204
Tyr Gly Asn Asn Arg Phe Pro Phe Phe Ser Ser Ser Ala Lys Ser His	
35 40 45	
ttt aaa aaa cca act caa gca tgt tta tcc tca aca acc cac caa gaa	252
Phe Lys Lys Pro Thr Gln Ala Cys Leu Ser Ser Thr Thr His Gln Glu	
50 55 60	
gtt cgt cca tta gca tac ttt cct cct act gtc tgg ggc aat cgc ttt	300
Val Arg Pro Leu Ala Tyr Phe Pro Pro Thr Val Trp Gly Asn Arg Phe	
65 70 75	
gct tcc ttg acc ttc aat cca tcg gaa ttt gaa tcg tat gat gaa cgg	348
Ala Ser Leu Thr Phe Asn Pro Ser Glu Phe Glu Ser Tyr Asp Glu Arg	
80 85 90	
gta att gtg ctg aag aaa aaa gtt aag gac ata tta att tca tct aca	396
Val Ile Val Leu Lys Lys Lys Val Lys Asp Ile Leu Ile Ser Ser Thr	
95 100 105 110	
agt gat tca gtg gag acc gtt att tta atc gac tta tta tgt cgg ctt	444
Ser Asp Ser Val Glu Thr Val Ile Leu Ile Asp Leu Leu Cys Arg Leu	
115 120 125	
ggc gta tca tat cac ttt gaa aat gat att gaa gag cta cta agt aaa	492
Gly Val Ser Tyr His Phe Glu Asn Asp Ile Glu Glu Leu Leu Ser Lys	
130 135 140	
atc ttc aac tcc cag cct gac ctt gtc gat gaa aaa gaa tgt gat ctc	540
Ile Phe Asn Ser Gln Pro Asp Leu Val Asp Glu Lys Glu Cys Asp Leu	
145 150 155	
tac act gcg gca att gta ttc cga gtt ttc aga cag cat ggt ttt aaa	588
Tyr Thr Ala Ala Ile Val Phe Arg Val Phe Arg Gln His Gly Phe Lys	
160 165 170	
atg tct tcg gat gtg ttt agc aaa ttc aag gac agt gat ggt aag ttc	636
Met Ser Ser Asp Val Phe Ser Lys Phe Lys Asp Ser Asp Gly Lys Phe	
175 180 185 190	
aag gaa tcc cta cgg ggt gat gct aag ggt atg ctc agc ctt ttt gaa	684
Lys Glu Ser Leu Arg Gly Asp Ala Lys Gly Met Leu Ser Leu Phe Glu	
195 200 205	
gct tcc cat cta agt gtg cat gga gaa gac att ctt gaa gaa gcc ttt	732
Ala Ser His Leu Ser Val His Gly Glu Asp Ile Leu Glu Glu Ala Phe	
210 215 220	
gct ttc acc aag gat tac tta cag tcc tct gca gtt gag tta ttc cct	780
Ala Phe Thr Lys Asp Tyr Leu Gln Ser Ser Ala Val Glu Leu Phe Pro	
225 230 235	



aat	ctc	aaa	agg	cat	ata	acg	aac	gcc	cta	gag	cag	cct	ttc	cac	agt	828
Asn	Leu	Lys	Arg	His	Ile	Thr	Asn	Ala	Leu	Glu	Gln	Pro	Phe	His	Ser	
ggc	gtg	ccg	agg	cta	gag	gcc	agg	aaa	ttc	atc	gat	cta	tac	gaa	gct	876
Gly	Val	Pro	Arg	Leu	Glu	Ala	Arg	Lys	Phe	Ile	Asp	Leu	Tyr	Glu	Ala	
gat	att	gaa	tgc	cgg	aat	gaa	act	ctg	ctc	gag	ttt	gca	aag	ttg	gat	924
Asp	Ile	Glu	Cys	Arg	Asn	Glu	Thr	Leu	Leu	Glu	Phe	Ala	Lys	Leu	Asp	
tat	aat	aga	gtt	cag	tta	ttg	cac	caa	caa	gag	ctg	tgc	cag	ttc	tca	972
Tyr	Asn	Arg	Val	Gln	Leu	Leu	His	Gln	Gln	Glu	Leu	Cys	Gln	Phe	Ser	
aag	tgg	tgg	aaa	gac	ctg	aat	ctt	gct	tcg	gat	att	cct	tat	gca	aga	1020
Lys	Trp	Trp	Lys	Asp	Leu	Asn	Leu	Ala	Ser	Asp	Ile	Pro	Tyr	Ala	Arg	
gac	aga	atg	gca	gag	att	ttc	ttt	tgg	gca	gtc	gcg	atg	tac	ttt	gag	1068
Asp	Arg	Met	Ala	Glu	Ile	Phe	Phe	Trp	Ala	Val	Ala	Met	Tyr	Phe	Glu	
cct	gac	tat	gca	cac	acc	cga	atg	att	att	gcg	aag	gtt	gta	ttg	ctt	1116
Pro	Asp	Tyr	Ala	His	Thr	Arg	Met	Ile	Ile	Ala	Lys	Val	Val	Leu	Leu	
ata	tca	cta	ata	gat	gat	aca	att	gat	gcg	tat	gca	aca	atg	gag	gaa	1164
Ile	Ser	Leu	Ile	Asp	Asp	Thr	Ile	Asp	Ala	Tyr	Ala	Thr	Met	Glu	Glu	
act	cat	att	ctt	gct	gaa	gca	gtc	gca	agg	tgg	gac	atg	agc	tgc	ctc	1212
Thr	His	Ile	Leu	Ala	Glu	Ala	Val	Ala	Arg	Trp	Asp	Met	Ser	Cys	Leu	
gag	aag	ctg	cca	gat	tac	atg	aaa	gtt	att	tat	aaa	cta	ttg	cta	aac	1260
Glu	Lys	Leu	Pro	Asp	Tyr	Met	Lys	Val	Ile	Tyr	Lys	Leu	Leu	Leu	Asn	
acc	ttc	tct	gaa	ttc	gag	aaa	gaa	ttg	acg	gcg	gaa	ggc	aag	tcc	tac	1308
Thr	Phe	Ser	Glu	Phe	Glu	Lys	Glu	Leu	Thr	Ala	Glu	Gly	Lys	Ser	Tyr	
agc	gtc	aaa	tac	gga	agg	gaa	gcg	ttt	caa	gaa	cta	gtg	aga	ggc	tac	1356
Ser	Val	Lys	Tyr	Gly	Arg	Glu	Ala	Phe	Gln	Glu	Leu	Val	Arg	Gly	Tyr	
tac	ctg	gag	gct	gta	tgg	cgc	gac	gag	ggc	aaa	ata	cca	tcg	ttc	gat	1404
Tyr	Leu	Glu	Ala	Val	Trp	Arg	Asp	Glu	Gly	Lys	Ile	Pro	Ser	Phe	Asp	
gac	tac	ttg	tat	aat	gga	tcc	atg	acc	acc	gga	ttg	cct	ctc	gtc	tca	1452
Asp	Tyr	Leu	Tyr	Asn	Gly	Ser	Met	Thr	Thr	Gly	Leu	Pro	Leu	Val	Ser	
aca	gct	tct	ttc	atg	gga	gtt	caa	gaa	att	aca	ggt	ctc	aac	gaa	ttc	1500

<400>	42															
Met	Ala	Leu	Pro	Ser	Ala	Ala	Met	Gln	Ser	Asn	Pro	Glu	Lys	Leu	Asn	
1				5					10					15		
Leu	Phe	His	Arg	Leu	Ser	Ser	Leu	Pro	Thr	Thr	Ser	Leu	Glu	Tyr	Gly	
			20					25					30			
Asn	Asn	Arg	Phe	Pro	Phe	Phe	Ser	Ser	Ser	Ala	Lys	Ser	His	Phe	Lys	
		35					40					45				
Lys	Pro	Thr	Gln	Ala	Cys	Leu	Ser	Ser	Thr	Thr	His	Gln	Glu	Val	Arg	
	50					55					60					
Pro	Leu	Ala	Tyr	Phe	Pro	Pro	Thr	Val	Trp	Gly	Asn	Arg	Phe	Ala	Ser	
65					70					75					80	
Leu	Thr	Phe	Asn	Pro	Ser	Glu	Phe	Glu	Ser	Tyr	Asp	Glu	Arg	Val	Ile	
				85					90					95		
Val	Leu	Lys	Lys	Lys	Val	Lys	Asp	Ile	Leu	Ile	Ser	Ser	Thr	Ser	Asp	

[illegible]

```
<210> 43
<211> 2700
<212> DNA
<213> Taxus brevifolia

<220>
<221> CDS
<222> (22)...(2607)
<223> taxadiene synthase
```

cDNA sequence																Position
<400>	43	ttccccctgcc	tctctggaga	a	atg	gct	cag	ctc	tca	ttt	aat	gca	gcg	ctg		51
					Met	Ala	Gln	Leu	Ser	Phe	Asn	Ala	Ala	Leu		
					1				5					10		
aag	atg	aac	gca	ttg	ggg	aac	aag	gca	atc	cac	gat	cca	acg	aat	tgc	99
Lys	Met	Asn	Ala	Leu	Gly	Asn	Lys	Ala	Ile	His	Asp	Pro	Thr	Asn	Cys	
				15					20					25		
aga	gcc	aaa	tct	gag	cgc	caa	atg	atg	tgg	gtt	tgc	tcc	aga	tca	ggg	147
Arg	Ala	Lys	Ser	Glu	Arg	Gln	Met	Met	Trp	Val	Cys	Ser	Arg	Ser	Gly	
			30					35					40			
cga	acc	aga	gta	aaa	atg	tcg	aga	gga	agt	ggg	ggg	cct	ggg	cct	gtc	195
Arg	Thr	Arg	Val	Lys	Met	Ser	Arg	Gly	Ser	Gly	Gly	Pro	Gly	Pro	Val	
		45					50					55				
gta	atg	atg	agc	agc	agc	act	ggc	act	agc	aag	gtg	gtt	tcc	gag	act	243
Val	Met	Met	Ser	Ser	Ser	Thr	Gly	Thr	Ser	Lys	Val	Val	Ser	Glu	Thr	
	60					65					70					
tcc	agt	acc	att	gtg	gat	gat	atc	cct	cga	ctc	tcc	gcc	aat	tat	cat	291
Ser	Ser	Thr	Ile	Val	Asp	Asp	Ile	Pro	Arg	Leu	Ser	Ala	Asn	Tyr	His	
	75				80					85					90	
ggc	gat	ctg	tgg	cac	cac	aat	gtt	ata	caa	act	ctg	gag	aca	ccg	ttt	339
Gly	Asp	Leu	Trp	His	His	Asn	Val	Ile	Gln	Thr	Leu	Glu	Thr	Pro	Phe	
				95					100					105		
cgt	gag	agt	tct	act	tac	caa	gaa	cgg	gca	gat	gag	ctg	gtt	gtg	aaa	387
Arg	Glu	Ser	Ser	Thr	Tyr	Gln	Glu	Arg	Ala	Asp	Glu	Leu	Val	Val	Lys	
			110					115					120			
att	aaa	gat	atg	ttc	aat	gcg	ctc	gga	gac	gga	gat	atc	agt	ccg	tct	435
Ile	Lys	Asp	Met	Phe	Asn	Ala	Leu	Gly	Asp	Gly	Asp	Ile	Ser	Pro	Ser	
		125					130					135				
gca	tac	gac	act	gcg	tgg	gtg	gcg	agg	ctg	gcg	acc	att	tcc	tct	gat	483
Ala	Tyr	Asp	Thr	Ala	Trp	Val	Ala	Arg	Leu	Ala	Thr	Ile	Ser	Ser	Asp	
	140					145					150					

gga Gly 155	tct Ser	gag Glu	aag Lys	cca Pro	cgg Arg 160	ttt Phe	cct Pro	cag Gln	gcc Ala	ctc Leu 165	aac Asn	tgg Trp	gtt Val	ttc Phe	aac Asn 170	531
aac Asn	cag Gln	ctc Leu	cag Gln	gat Asp 175	gga Gly	tcg Ser	tgg Trp	ggt Gly	atc Ile 180	gaa Glu	tcg Ser	cac His	ttt Phe	agt Ser 185	tta Leu	579
tgc Cys	gat Asp	cga Arg	ttg Leu 190	ctt Leu	aac Asn	acg Thr	acc Thr	aat Asn 195	tct Ser	gtt Val	atc Ile	gcc Ala 200	ctc Leu	tcg Ser	gtt Val	627
tgg Trp	aaa Lys	aca Thr 205	ggg Gly	cac His	agc Ser	caa Gln	gta Val 210	caa Gln	caa Gln	ggt Gly	gct Ala 215	gag Glu	ttt Phe	att Ile	gca Ala	675
gag Glu	aat Asn 220	cta Leu	aga Arg	tta Leu	ctc Leu	aat Asn 225	gag Glu	gaa Glu	gat Asp	gag Glu 230	ttg Leu	tcc Ser	ccg Pro	gat Asp	ttc Phe	723
caa Gln 235	ata Ile	atc Ile	ttt Phe	cct Pro	gct Ala 240	ctg Leu	ctg Leu	caa Gln	aag Lys	gca Ala 245	aaa Lys	gcg Ala	ttg Leu	ggg Gly	atc Ile 250	771
aat Asn	ctt Leu	cct Pro	tac Tyr	gat Asp 255	ctt Leu	cca Pro	ttt Phe	atc Ile	aaa Lys 260	tat Tyr	ttg Leu	tcg Ser	aca Thr	aca Thr 265	cgg Arg	819
gaa Glu	gcc Ala	agg Arg	ctt Leu 270	aca Thr	gat Asp	gtt Val	tct Ser	gcg Ala 275	gca Ala	gca Ala	gac Asp	aat Asn 280	att Ile	cca Pro	gcc Ala	867
aac Asn	atg Met	ttg Leu 285	aat Asn	gcg Ala	ttg Leu	gaa Glu	ggt Gly 290	ctc Leu	gag Glu	gaa Glu	gtt Val	att Ile 295	gac Asp	tgg Trp	aac Asn	915
aag Lys	att Ile 300	atg Met	agg Arg	ttt Phe	caa Gln	agt Ser 305	aaa Lys	gat Asp	gga Gly	tct Ser	ttc Phe 310	ctg Leu	agc Ser	tcc Ser	cct Pro	963
gcc Ala 315	tcc Ser	act Thr	gcc Ala	tgt Cys	gta Val 320	ctg Leu	atg Met	aat Asn	aca Thr	ggg Gly 325	gac Asp	gaa Glu	aaa Lys	tgt Cys	ttc Phe 330	1011
act Thr	ttt Phe	ctc Leu	aac Asn	aat Asn 335	ctg Leu	ctc Leu	gac Asp	aaa Lys	ttc Phe 340	ggc Gly	ggc Gly	tgc Cys	gtg Val	ccc Pro 345	tgt Cys	1059
atg Met	tat Tyr	tcc Ser	atc Ile 350	gat Asp	ctg Leu	ctg Leu	gaa Glu	cgc Arg 355	ott Leu	tcg Ser	ctg Leu	gtt Val	gat Asp 360	aac Asn	att Ile	1107
gag Glu	cat His	ctc Leu 365	gga Gly	atc Ile	ggt Gly	cgc Arg	cat His 370	ttc Phe	aaa Lys	caa Gln	gaa Glu	atc Ile 375	aaa Lys	gga Gly	gct Ala	1155

ctt gat tat gtc tac aga cat tgg agt gaa agg ggc atc ggt tgg ggc Leu Asp Tyr Val Tyr Arg His Trp Ser Glu Arg Gly Ile Gly Trp Gly 380 385 390	1203
aga gac agc ctt gtt cca gat ctc aac acc aca gcc ctc ggc ctg cga Arg Asp Ser Leu Val Pro Asp Leu Asn Thr Thr Ala Leu Gly Leu Arg 395 400 405 410	1251
act ctt cgc atg cac gga tac aat gtt tct tca gac gtt ttg aat aat Thr Leu Arg Met His Gly Tyr Asn Val Ser Ser Asp Val Leu Asn Asn 415 420 425	1299
ttc aaa gat gaa aac ggg cgg ttc ttc tcc tct gcg ggc caa acc cat Phe Lys Asp Glu Asn Gly Arg Phe Phe Ser Ser Ala Gly Gln Thr His 430 435 440	1347
gtc gaa ttg aga agc gtg gtg aat ctt ttc aga gct tcc gac ctt gca Val Glu Leu Arg Ser Val Val Asn Leu Phe Arg Ala Ser Asp Leu Ala 445 450 455	1395
ttt cct gac gaa aga gct atg gac gat gct aga aaa ttt gca gaa cca Phe Pro Asp Glu Arg Ala Met Asp Asp Ala Arg Lys Phe Ala Glu Pro 460 465 470	1443
tat ctt aga gag gca ctt gca acg aaa atc tca acc aat aca aaa cta Tyr Leu Arg Glu Ala Leu Ala Thr Lys Ile Ser Thr Asn Thr Lys Leu 475 480 485 490	1491
ttc aaa gag att gag tac gtg gtg gag tac cct tgg cac atg agt atc Phe Lys Glu Ile Glu Tyr Val Val Glu Tyr Pro Trp His Met Ser Ile 495 500 505	1539
cca cgc tta gaa gcc aga agt tat att gat tca tat gac gac aat tat Pro Arg Leu Glu Ala Arg Ser Tyr Ile Asp Ser Tyr Asp Asp Asn Tyr 510 515 520	1587
gta tgg cag agg aag act cta tat aga atg cca tct ttg agt aat tca Val Trp Gln Arg Lys Thr Leu Tyr Arg Met Pro Ser Leu Ser Asn Ser 525 530 535	1635
aaa tgt tta gaa ttg gca aaa ttg gac ttc aat atc gta caa tct ttg Lys Cys Leu Glu Leu Ala Lys Leu Asp Phe Asn Ile Val Gln Ser Leu 540 545 550	1683
cat caa gag gag ttg aag ctt cta aca aga tgg tgg aag gaa tcc ggc His Gln Glu Glu Leu Lys Leu Leu Thr Arg Trp Trp Lys Glu Ser Gly 555 560 565 570	1731
atg gca gat ata aat ttc act cga cac cga gtg gcg gag gtt tat ttt Met Ala Asp Ile Asn Phe Thr Arg His Arg Val Ala Glu Val Tyr Phe 575 580 585	1779
tca tca gct aca ttt gaa ccc gaa tat tct gcc act aga att gcc ttc Ser Ser Ala Thr Phe Glu Pro Glu Tyr Ser Ala Thr Arg Ile Ala Phe 590 595 600	1827
aca aaa att ggt tgt tta caa gtc ctt ttt gat gat atg gct gac atc	1875

T00000"000000000

Thr	Lys	Ile 605	Gly	Cys	Leu	Gln 610	Val	Leu	Phe	Asp	Asp	Met 615	Ala	Asp	Ile	
ttt Phe	gca Ala 620	aca Thr	cta Leu	gat Asp	gaa Glu 625	ttg Leu	aaa Lys	agt Ser	ttc Phe	act Thr	gag Glu 630	gga Gly	gta Val	aag Lys	aga Arg	1923
tgg Trp 635	gat Asp	aca Thr	tct Ser	ttg Leu 640	cta Leu	cat His	gag Glu	att Ile	cca Pro	gag Glu 645	tgt Cys	atg Met	caa Gln	act Thr	tgc Cys 650	1971
ttt Phe	aaa Lys	gtt Val	tgg Trp	ttc Phe 655	aaa Lys	tta Leu	atg Met	gaa Glu 660	gaa Glu	gta Val	aat Asn	aat Asn	gat Asp 665	gtg Val	gtt Val	2019
aag Lys	gta Val	caa Gln	gga Gly 670	cgt Arg	gac Asp	atg Met	ctc Leu 675	gct Ala	cac His	ata Ile	aga Arg	aaa Lys 680	ccc Pro	tgg Trp	gag Glu	2067
ttg Leu	tac Tyr 685	ttc Phe	aat Asn	tgt Cys	tat Tyr	gta Val 690	caa Gln	gaa Glu	agg Arg	gag Glu	tgg Trp 695	ctt Leu	gaa Glu	gcc Ala	ggg Gly	2115
tat Tyr	ata Ile 700	cca Pro	act Thr	ttt Phe	gaa Glu 705	gag Glu	tac Tyr	tta Leu	aag Lys	act Thr 710	tat Tyr	gct Ala	ata Ile	tca Ser	gta Val	2163
ggc Gly 715	ctt Leu	gga Gly	ccg Pro	tgt Cys 720	acc Thr	cta Leu	caa Gln	cca Pro	ata Ile	cta Leu 725	cta Leu	atg Met	ggg Gly	gag Glu	ctt Leu 730	2211
gtg Val	aaa Lys	gat Asp	gat Asp	gtt Val 735	gtt Val	gag Glu	aaa Lys	gtg Val 740	cac His	tat Tyr	ccc Pro	tca Ser	aat Asn	atg Met 745	ttt Phe	2259
gag Glu	ctt Leu	gta Val	tcc Ser 750	ttg Leu	agc Ser	tgg Trp	cga Arg 755	cta Leu	aca Thr	aac Asn	gac Asp	acc Thr 760	aaa Lys	aca Thr	tat Tyr	2307
cag Gln	gct Ala 765	gaa Glu	aag Lys	gct Ala	cga Arg	gga Gly 770	caa Gln	caa Gln	gcc Ala	tca Ser	ggc Gly 775	ata Ile	gca Ala	tgc Cys	tat Tyr	2355
atg Met	aag Lys 780	gat Asp	aat Asn	cca Pro	gga Gly	gca Ala 785	act Thr	gag Glu	gaa Glu	gat Asp 790	gcc Ala	att Ile	aag Lys	cac His	ata Ile	2403
tgt Cys 795	cgt Arg	gtt Val	gtt Val	gat Asp 800	cgg Arg	gcc Ala	ttg Leu	aaa Lys	gaa Glu 805	gca Ala	agc Ser	ttt Phe	gaa Glu	tat Tyr	ttc Phe 810	2451
aaa Lys	cca Pro	tcc Ser	aat Asn 815	gat Asp	atc Ile	cca Pro	atg Met	ggg Gly 820	tgc Cys	aag Lys	tcc Ser	ttt Phe	att Ile	ttt Phe 825	aac Asn	2499
ctt Leu	aga Arg	ttg Leu	tgt Cys	gtc Val	caa Gln	atc Ile	ttt Phe	tac Tyr	aag Lys	ttt Phe	ata Ile	gat Asp	ggg Gly	tac Tyr	gga Gly	2547

830	835	840	
atc gcc aat gag gag att aag gac tat ata aga aaa gtt tat att gat			2595
Ile Ala Asn Glu Glu Ile Lys Asp Tyr Ile Arg Lys Val Tyr Ile Asp			
845	850	855	
cca att caa gta tga tatatcatgt aaaacctctt ttatcatgata aattgactta			2650
Pro Ile Gln Val			
860			
ttattgtatt ggcaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa			2700

&lt;210&gt; 44

&lt;211&gt; 862

&lt;212&gt; PRT

<213> *Taxus brevifolia*

&lt;400&gt; 44

Met	Ala	Gln	Leu	Ser	Phe	Asn	Ala	Ala	Leu	Lys	Met	Asn	Ala	Leu	Gly
1				5					10					15	
Asn	Lys	Ala	Ile	His	Asp	Pro	Thr	Asn	Cys	Arg	Ala	Lys	Ser	Glu	Arg
		20						25				30			
Gln	Met	Met	Trp	Val	Cys	Ser	Arg	Ser	Gly	Arg	Thr	Arg	Val	Lys	Met
	35						40				45				
Ser	Arg	Gly	Ser	Gly	Gly	Pro	Gly	Pro	Val	Val	Met	Met	Ser	Ser	Ser
	50					55				60					
Thr	Gly	Thr	Ser	Lys	Val	Val	Ser	Glu	Thr	Ser	Ser	Thr	Ile	Val	Asp
65					70					75					80
Asp	Ile	Pro	Arg	Leu	Ser	Ala	Asn	Tyr	His	Gly	Asp	Leu	Trp	His	His
				85					90					95	
Asn	Val	Ile	Gln	Thr	Leu	Glu	Thr	Pro	Phe	Arg	Glu	Ser	Ser	Thr	Tyr
			100					105					110		
Gln	Glu	Arg	Ala	Asp	Glu	Leu	Val	Val	Lys	Ile	Lys	Asp	Met	Phe	Asn
		115					120					125			
Ala	Leu	Gly	Asp	Gly	Asp	Ile	Ser	Pro	Ser	Ala	Tyr	Asp	Thr	Ala	Trp
	130					135					140				
Val	Ala	Arg	Leu	Ala	Thr	Ile	Ser	Ser	Asp	Gly	Ser	Glu	Lys	Pro	Arg
145					150					155					160
Phe	Pro	Gln	Ala	Leu	Asn	Trp	Val	Phe	Asn	Asn	Gln	Leu	Gln	Asp	Gly
			165						170					175	
Ser	Trp	Gly	Ile	Glu	Ser	His	Phe	Ser	Leu	Cys	Asp	Arg	Leu	Leu	Asn
		180						185					190		
Thr	Thr	Asn	Ser	Val	Ile	Ala	Leu	Ser	Val	Trp	Lys	Thr	Gly	His	Ser
		195					200					205			
Gln	Val	Gln	Gln	Gly	Ala	Glu	Phe	Ile	Ala	Glu	Asn	Leu	Arg	Leu	Leu
	210					215					220				
Asn	Glu	Glu	Asp	Glu	Leu	Ser	Pro	Asp	Phe	Gln	Ile	Ile	Phe	Pro	Ala
225					230					235					240
Leu	Leu	Gln	Lys	Ala	Lys	Ala	Leu	Gly	Ile	Asn	Leu	Pro	Tyr	Asp	Leu
			245						250					255	
Pro	Phe	Ile	Lys	Tyr	Leu	Ser	Thr	Thr	Arg	Glu	Ala	Arg	Leu	Thr	Asp
		260						265					270		
Val	Ser	Ala	Ala	Ala	Asp	Asn	Ile	Pro	Ala	Asn	Met	Leu	Asn	Ala	Leu
		275					280					285			
Glu	Gly	Leu	Glu	Glu	Val	Ile	Asp	Trp	Asn	Lys	Ile	Met	Arg	Phe	Gln
	290					295				300					
Ser	Lys	Asp	Gly	Ser	Phe	Leu	Ser	Ser	Pro	Ala	Ser	Thr	Ala	Cys	Val

F08990.02826860



305					310					315					320	
Leu	Met	Asn	Thr	Gly	Asp	Glu	Lys	Cys	Phe	Thr	Phe	Leu	Asn	Asn	Leu	
				325					330					335		
Leu	Asp	Lys	Phe	Gly	Gly	Cys	Val	Pro	Cys	Met	Tyr	Ser	Ile	Asp	Leu	
			340					345					350			
Leu	Glu	Arg	Leu	Ser	Leu	Val	Asp	Asn	Ile	Glu	His	Leu	Gly	Ile	Gly	
		355					360					365				
Arg	His	Phe	Lys	Gln	Glu	Ile	Lys	Gly	Ala	Leu	Asp	Tyr	Val	Tyr	Arg	
	370					375					380					
His	Trp	Ser	Glu	Arg	Gly	Ile	Gly	Trp	Gly	Arg	Asp	Ser	Leu	Val	Pro	
385					390					395					400	
Asp	Leu	Asn	Thr	Thr	Ala	Leu	Gly	Leu	Arg	Thr	Leu	Arg	Met	His	Gly	
				405					410					415		
Tyr	Asn	Val	Ser	Ser	Asp	Val	Leu	Asn	Asn	Phe	Lys	Asp	Glu	Asn	Gly	
			420					425					430			
Arg	Phe	Phe	Ser	Ser	Ala	Gly	Gln	Thr	His	Val	Glu	Leu	Arg	Ser	Val	
		435				440						445				
Val	Asn	Leu	Phe	Arg	Ala	Ser	Asp	Leu	Ala	Phe	Pro	Asp	Glu	Arg	Ala	
	450				455						460					
Met	Asp	Asp	Ala	Arg	Lys	Phe	Ala	Glu	Pro	Tyr	Leu	Arg	Glu	Ala	Leu	
465					470					475					480	
Ala	Thr	Lys	Ile	Ser	Thr	Asn	Thr	Lys	Leu	Phe	Lys	Glu	Ile	Glu	Tyr	
				485					490					495		
Val	Val	Glu	Tyr	Pro	Trp	His	Met	Ser	Ile	Pro	Arg	Leu	Glu	Ala	Arg	
			500					505					510			
Ser	Tyr	Ile	Asp	Ser	Tyr	Asp	Asp	Asn	Tyr	Val	Trp	Gln	Arg	Lys	Thr	
		515					520					525				
Leu	Tyr	Arg	Met	Pro	Ser	Leu	Ser	Asn	Ser	Lys	Cys	Leu	Glu	Leu	Ala	
	530					535					540					
Lys	Leu	Asp	Phe	Asn	Ile	Val	Gln	Ser	Leu	His	Gln	Glu	Glu	Leu	Lys	
545					550					555					560	
Leu	Leu	Thr	Arg	Trp	Trp	Lys	Glu	Ser	Gly	Met	Ala	Asp	Ile	Asn	Phe	
				565					570					575		
Thr	Arg	His	Arg	Val	Ala	Glu	Val	Tyr	Phe	Ser	Ser	Ala	Thr	Phe	Glu	
			580					585					590			
Pro	Glu	Tyr	Ser	Ala	Thr	Arg	Ile	Ala	Phe	Thr	Lys	Ile	Gly	Cys	Leu	
		595					600					605				
Gln	Val	Leu	Phe	Asp	Asp	Met	Ala	Asp	Ile	Phe	Ala	Thr	Leu	Asp	Glu	
	610					615					620					
Leu	Lys	Ser	Phe	Thr	Glu	Gly	Val	Lys	Arg	Trp	Asp	Thr	Ser	Leu	Leu	
625					630					635					640	
His	Glu	Ile	Pro	Glu	Cys	Met	Gln	Thr	Cys	Phe	Lys	Val	Trp	Phe	Lys	
				645					650					655		
Leu	Met	Glu	Glu	Val	Asn	Asn	Asp	Val	Val	Lys	Val	Gln	Gly	Arg	Asp	
			660													

Gly Gln Gln Ala Ser Gly Ile Ala Cys Tyr Met Lys Asp Asn Pro Gly  
 770 775 780  
 Ala Thr Glu Glu Asp Ala Ile Lys His Ile Cys Arg Val Val Asp Arg  
 785 790 795 800  
 Ala Leu Lys Glu Ala Ser Phe Glu Tyr Phe Lys Pro Ser Asn Asp Ile  
 805 810 815  
 Pro Met Gly Cys Lys Ser Phe Ile Phe Asn Leu Arg Leu Cys Val Gln  
 820 825 830  
 Ile Phe Tyr Lys Phe Ile Asp Gly Tyr Gly Ile Ala Asn Glu Glu Ile  
 835 840 845  
 Lys Asp Tyr Ile Arg Lys Val Tyr Ile Asp Pro Ile Gln Val  
 850 855 860

&lt;210&gt; 45

&lt;211&gt; 2424

&lt;212&gt; DNA

<213> *Abies grandis*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (2)...(2347)

&lt;223&gt; E-alpha-bisabolene synthase

&lt;400&gt; 45

g ggt tat gat ctt gtg cat tct ctt aaa tca cct tat att gat tct agt 49  
 Gly Tyr Asp Leu Val His Ser Leu Lys Ser Pro Tyr Ile Asp Ser Ser  
 1 5 10 15  
 tac aga gaa cgc gcg gag gtc ctt gtt agc gag att aaa gtg atg ctt 97  
 Tyr Arg Glu Arg Ala Glu Val Leu Val Ser Glu Ile Lys Val Met Leu  
 20 25 30  
 aat cca gct att aca gga gat gga gaa tca atg att act cca tct gct 145  
 Asn Pro Ala Ile Thr Gly Asp Gly Glu Ser Met Ile Thr Pro Ser Ala  
 35 40 45  
 tat gac aca gca tgg gta gcg agg gtg ccc gcc att gat ggc tct gct 193  
 Tyr Asp Thr Ala Trp Val Ala Arg Val Pro Ala Ile Asp Gly Ser Ala  
 50 55 60  
 cgc ccg caa ttt ccc caa aca gtt gac tgg att ttg aaa aac cag tta 241  
 Arg Pro Gln Phe Pro Gln Thr Val Asp Trp Ile Leu Lys Asn Gln Leu  
 65 70 75 80  
 aaa gat ggt tca tgg gga att cag tcc cac ttt ctg ctg tcc gac cgt 289  
 Lys Asp Gly Ser Trp Gly Ile Gln Ser His Phe Leu Leu Ser Asp Arg  
 85 90 95  
 ctt ctt gcc act ctt tct tgt gtt ctt gtg ctc ctt aaa tgg aac gtt 337  
 Leu Leu Ala Thr Leu Ser Cys Val Leu Val Leu Leu Lys Trp Asn Val  
 100 105 110  
 ggg gat ctg caa gta gag cag gga att gaa ttc ata aag agc aat ctg 385  
 Gly Asp Leu Gln Val Glu Gln Gly Ile Glu Phe Ile Lys Ser Asn Leu  
 115 120 125  
 gaa cta gta aag gat gaa acc gat caa gat agc ttg gta aca gac ttt 433

F02390-0235660

Glu	Leu	Val	Lys	Asp	Glu	Thr	Asp	Gln	Asp	Ser	Leu	Val	Thr	Asp	Phe		
130						135					140						
gag	atc	ata	ttt	cct	tct	ctg	tta	aga	gaa	gct	caa	tct	ctg	cgc	ctc	481	
Glu	Ile	Ile	Phe	Pro	Ser	Leu	Leu	Arg	Glu	Ala	Gln	Ser	Leu	Arg	Leu		
145					150				155						160		
gga	ctt	ccc	tac	gac	ctg	cct	tat	ata	cat	ctg	ttg	cag	act	aaa	cgg	529	
Gly	Leu	Pro	Tyr	Asp	Leu	Pro	Tyr	Ile	His	Leu	Leu	Gln	Thr	Lys	Arg		
				165					170					175			
cag	gaa	aga	tta	gca	aaa	ctt	tca	agg	gag	gaa	att	tat	gcg	gtt	ccg	577	
Gln	Glu	Arg	Leu	Ala	Lys	Leu	Ser	Arg	Glu	Glu	Ile	Tyr	Ala	Val	Pro		
			180					185					190				
tcg	cca	ttg	ttg	tat	tct	tta	gag	gga	ata	caa	gat	ata	gtt	gaa	tgg	625	
Ser	Pro	Leu	Leu	Tyr	Ser	Leu	Glu	Gly	Ile	Gln	Asp	Ile	Val	Glu	Trp		
		195				200						205					
gaa	cga	ata	atg	gaa	gtt	caa	agt	cag	gat	ggg	tct	ttc	tta	agc	tca	673	
Glu	Arg	Ile	Met	Glu	Val	Gln	Ser	Gln	Asp	Gly	Ser	Phe	Leu	Ser	Ser		
	210					215				220							
cct	gct	tct	act	gcc	tgc	gtt	ttc	atg	cac	aca	gga	gac	gcg	aaa	tgc	721	
Pro	Ala	Ser	Thr	Ala	Cys	Val	Phe	Met	His	Thr	Gly	Asp	Ala	Lys	Cys		
225					230					235					240		
ctt	gaa	ttc	ttg	aac	agt	gtg	atg	atc	aag	ttt	gga	aat	ttt	gtt	ccc	769	
Leu	Glu	Phe	Leu	Asn	Ser	Val	Met	Ile	Lys	Phe	Gly	Asn	Phe	Val	Pro		
				245					250					255			
tgc	ctg	tat	cct	gtg	gat	ctg	ctg	gaa	cgc	ctg	ttg	atc	gta	gat	aat	817	
Cys	Leu	Tyr	Pro	Val	Asp	Leu	Leu	Glu	Arg	Leu	Leu	Ile	Val	Asp	Asn		
			260					265					270				
att	gta	cgc	ctt	gga	atc	tat	aga	cac	ttt	gaa	aag	gaa	atc	aag	gaa	865	
Ile	Val	Arg	Leu	Gly	Ile	Tyr	Arg	His	Phe	Glu	Lys	Glu	Ile	Lys	Glu		
		275					280					285					
gct	ctt	gat	tat	gtt	tac	agg	cat	tgg	aac	gaa	aga	gga	att	ggg	tgg	913	
Ala	Leu	Asp	Tyr	Val	Tyr	Arg	His	Trp	Asn	Glu	Arg	Gly	Ile	Gly	Trp		
	290					295				300							
ggc	aga	cta	aat	ccc	ata	gca	gat	ctt	gag	acc	act	gct	ttg	gga	ttt	961	
Gly	Arg	Leu	Asn	Pro	Ile	Ala	Asp	Leu	Glu	Thr	Thr	Ala	Leu	Gly	Phe		
305					310				315						320		
cga	ttg	ctt	cgg	ctg	cat	agg	tac	aat	gta	tct	cca	gcc	att	ttt	gac	1009	
Arg	Leu	Leu	Arg	Leu	His	Arg	Tyr	Asn	Val	Ser	Pro	Ala	Ile	Phe	Asp		
				325					330					335			
aac	ttc	aaa	gat	gcc	aat	ggg	aaa	ttc	att	tgc	tcg	acc	ggt	caa	ttc	1057	
Asn	Phe	Lys	Asp	Ala	Asn	Gly	Lys	Phe	Ile	Cys	Ser	Thr	Gly	Gln	Phe		
			340					345					350				
aac	aaa	gat	gta	gca	agc	atg	ctg	aat	ctt	tat	aga	gct	tcc	cag	ctc	1105	
Asn	Lys	Asp	Val	Ala	Ser	Met	Leu	Asn	Leu	Tyr	Arg	Ala	Ser	Gln	Leu		

T00000-000000

355	360	365	
gca ttt ccc gga gaa aac att ctt gat gaa gct aaa agc ttc gct act Ala Phe Pro Gly Glu Asn Ile Leu Asp Glu Ala Lys Ser Phe Ala Thr 370 375 380			1153
aaa tat ttg aga gaa gct ctt gag aaa agt gag act tcc agt gca tgg Lys Tyr Leu Arg Glu Ala Leu Glu Lys Ser Glu Thr Ser Ser Ala Trp 385 390 395 400			1201
aac aac aaa caa aac ctg agc caa gag atc aaa tac gcg ctg aag act Asn Asn Lys Gln Asn Leu Ser Gln Glu Ile Lys Tyr Ala Leu Lys Thr 405 410 415			1249
tct tgg cat gcc agt gtt ccg aga gtg gaa gca aag aga tac tgt caa Ser Trp His Ala Ser Val Pro Arg Val Glu Ala Lys Arg Tyr Cys Gln 420 425 430			1297
gtg tat cgc cca gat tat gca cgc ata gca aaa tgc gtt tac aag cta Val Tyr Arg Pro Asp Tyr Ala Arg Ile Ala Lys Cys Val Tyr Lys Leu 435 440 445			1345
ccc tac gtg aac aat gaa aag ttt tta gag ctg gga aaa tta gat ttc Pro Tyr Val Asn Asn Glu Lys Phe Leu Glu Leu Gly Lys Leu Asp Phe 450 455 460			1393
aac att atc cag tcc atc cac caa gaa gaa atg aag aat gtt acc agc Asn Ile Ile Gln Ser Ile His Gln Glu Glu Met Lys Asn Val Thr Ser 465 470 475 480			1441
tgg ttt aga gat tcg ggg ttg cca cta ttc acc ttc gct cgg gag agg Trp Phe Arg Asp Ser Gly Leu Pro Leu Phe Thr Phe Ala Arg Glu Arg 485 490 495			1489
ccg ctg gaa ttc tac ttc tta gta gcg gcg ggg acc tat gaa ccc cag Pro Leu Glu Phe Tyr Phe Leu Val Ala Ala Gly Thr Tyr Glu Pro Gln 500 505 510			1537
tat gcc aaa tgc agg ttc ctc ttt aca aaa gtg gca tgc ttg cag act Tyr Ala Lys Cys Arg Phe Leu Phe Thr Lys Val Ala Cys Leu Gln Thr 515 520 525			1585
gtt ctg gac gat atg tat gac act tat gga acc cta gat gaa ttg aag Val Leu Asp Asp Met Tyr Asp Thr Tyr Gly Thr Leu Asp Glu Leu Lys 530 535 540			1633
cta ttc act gag gct gtg aga aga tgg gac ctc tcc ttt aca gaa aac Leu Phe Thr Glu Ala Val Arg Arg Trp Asp Leu Ser Phe Thr Glu Asn 545 550 555 560			1681
ctt cca gac tat atg aaa cta tgt tac caa atc tat tat gac ata gtt Leu Pro Asp Tyr Met Lys Leu Cys Tyr Gln Ile Tyr Tyr Asp Ile Val 565 570 575			1729
cac gag gtg gct tgg gag gca gag aag gaa cag ggg cgt gaa ttg gtc His Glu Val Ala Trp Glu Ala Glu Lys Glu Gln Gly Arg Glu Leu Val 580 585 590			1777

T08230"0286650

agc ttt ttc aga aag gga tgg gag gat tat ctt ctg ggt tat tat gaa 1825  
 Ser Phe Phe Arg Lys Gly Trp Glu Asp Tyr Leu Leu Gly Tyr Tyr Glu  
 595 600 605  
  
 gaa gct gaa tgg tta gct gct gag tat gtg cct acc ttg gac gag tac 1873  
 Glu Ala Glu Trp Leu Ala Ala Glu Tyr Val Pro Thr Leu Asp Glu Tyr  
 610 615 620  
  
 ata aag aat gga atc aca tct atc ggc caa cgt ata ctt ctg ttg agt 1921  
 Ile Lys Asn Gly Ile Thr Ser Ile Gly Gln Arg Ile Leu Leu Leu Ser  
 625 630 635 640  
  
 gga gtg ttg ata atg gat ggg caa ctc ctt tcg caa gag gca tta gag 1969  
 Gly Val Leu Ile Met Asp Gly Gln Leu Leu Ser Gln Glu Ala Leu Glu  
 645 650 655  
  
 aaa gta gat tat cca gga aga cgt gtt ctc aca gag ctg aat agc ctc 2017  
 Lys Val Asp Tyr Pro Gly Arg Arg Val Leu Thr Glu Leu Asn Ser Leu  
 660 665 670  
  
 att tcc cgc ctg gcg gat gac acg aag aca tat aaa gct gag aag gct 2065  
 Ile Ser Arg Leu Ala Asp Asp Thr Lys Thr Tyr Lys Ala Glu Lys Ala  
 675 680 685  
  
 cgt gga gaa ttg gcg tcc agc att gaa tgt tac atg aaa gac cat cct 2113  
 Arg Gly Glu Leu Ala Ser Ser Ile Glu Cys Tyr Met Lys Asp His Pro  
 690 695 700  
  
 gaa tgt aca gag gaa gag gct ctc gat cac atc tat agc att ctg gag 2161  
 Glu Cys Thr Glu Glu Glu Ala Leu Asp His Ile Tyr Ser Ile Leu Glu  
 705 710 715 720  
  
 ccg gcg gtg aag gaa ctg aca aga gag ttt ctg aag ccc gac gac gtc 2209  
 Pro Ala Val Lys Glu Leu Thr Arg Glu Phe Leu Lys Pro Asp Asp Val  
 725 730 735  
  
 cca ttc gcc tgc aag aag atg ctt ttc gag gag aca aga gtg acg atg 2257  
 Pro Phe Ala Cys Lys Lys Met Leu Phe Glu Glu Thr Arg Val Thr Met  
 740 745 750  
  
 gtg ata ttc aag gat gga gat gga ttc ggt gtt tcc aaa tta gaa gtc 2305  
 Val Ile Phe Lys Asp Gly Asp Gly Phe Gly Val Ser Lys Leu Glu Val  
 755 760 765  
  
 aaa gat cat atc aaa gag tgt ctc att gaa ccg ctg cca ctg taa 2350  
 Lys Asp His Ile Lys Glu Cys Leu Ile Glu Pro Leu Pro Leu  
 770 775 780  
  
 tcaaaaatagt tgcaataata attgaaataa tgtcaactat gtttcacaaa aaaaaaaaaa 2410  
 aaaaaaaaaa aaaa 2424

<210> 46  
 <211> 782  
 <212> PRT  
 <213> Abies grandis

F03290"0232860

Gly 1	Tyr	Asp	Leu	Val 5	His	Ser	Leu	Lys	Ser 10	Pro	Tyr	Ile	Asp	Ser 15	Ser
Tyr	Arg	Glu	Arg	Ala 20	Glu	Val	Leu	Val 25	Ser	Glu	Ile	Lys	Val 30	Met	Leu
Asn	Pro	Ala	Ile	Thr 35	Gly	Asp	Gly	Glu 40	Ser	Met	Ile	Thr	Pro 45	Ser	Ala
Tyr	Asp	Thr	Ala	Trp 50	Val	Ala	Arg	Val 55	Pro	Ala	Ile	Asp	Gly 60	Ser	Ala
Arg 65	Pro	Gln	Phe	Pro 70	Gln	Thr	Val	Asp 75	Trp	Ile	Leu	Lys	Asn 80	Gln	Leu
Lys	Asp	Gly	Ser	Trp 85	Gly	Ile	Gln	Ser 90	His	Phe	Leu	Leu	Ser 95	Asp	Arg
Leu	Leu	Ala	Thr	Leu 100	Ser	Cys	Val	Leu 105	Val	Leu	Leu	Lys	Trp 110	Asn	Val
Gly	Asp	Leu	Gln	Val 115	Glu	Gln	Gly	Ile 120	Glu	Phe	Ile	Lys	Ser 125	Asn	Leu
Glu	Leu	Val	Lys	Asp 130	Glu	Thr	Asp	Gln 135	Asp	Ser	Leu	Val	Thr 140	Asp	Phe
Glu 145	Ile	Ile	Phe	Pro 150	Ser	Leu	Leu	Arg 155	Glu	Ala	Gln	Ser	Leu 160	Arg	Leu
Gly	Leu	Pro	Tyr	Asp 165	Leu	Pro	Tyr	Ile 170	His	Leu	Leu	Gln	Thr 175	Lys	Arg
Gln	Glu	Arg	Leu	Ala 180	Lys	Leu	Ser	Arg 185	Glu	Glu	Ile	Tyr	Ala 190	Val	Pro
Ser	Pro	Leu	Leu	Tyr 195	Ser	Leu	Glu	Gly 200	Ile	Gln	Asp	Ile	Val 205	Glu	Trp
Glu	Arg	Ile	Met	Glu 210	Val	Gln	Ser	Gln 215	Asp	Gly	Ser	Phe	Leu 220	Ser	Ser
Pro 225	Ala	Ser	Thr	Ala 230	Cys	Val	Phe	Met 235	His	Thr	Gly	Asp	Ala 240	Lys	Cys
Leu	Glu	Phe	Leu	Asn 245	Ser	Val	Met	Ile 250	Lys	Phe	Gly	Asn	Phe 255	Val	Pro
Cys	Leu	Tyr	Pro	Val 260	Asp	Leu	Leu	Glu 265	Arg	Leu	Leu	Ile	Val 270	Asp	Asn
Ile	Val	Arg	Leu	Gly 275	Ile	Tyr	Arg	His 280	Phe	Glu	Lys	Glu	Ile 285	Lys	Glu
Ala	Leu	Asp	Tyr	Val 290	Tyr	Arg	His	Trp 295	Asn	Glu	Arg	Gly	Ile 300	Gly	Trp
Gly 305	Arg	Leu	Asn	Pro 310	Ile	Ala	Asp	Leu 315	Glu	Thr	Thr	Ala	Leu 320	Gly	Phe
Arg	Leu	Leu	Arg	Leu 325	His	Arg	Tyr	Asn 330	Val	Ser	Pro	Ala	Ile 335	Phe	Asp
Asn	Phe	Lys	Asp	Ala 340	Asn	Gly	Lys	Phe 345	Ile	Cys	Ser	Thr	Gly 350	Gln	Phe
Asn	Lys	Asp	Val	Ala 355	Ser	Met	Leu	Asn 360	Leu	Tyr	Arg	Ala	Ser 365	Gln	Leu
Ala	Phe	Pro	Gly	Glu 370	Asn	Ile	Leu	Asp 375	Glu	Ala	Lys	Ser	Phe 380	Ala	Thr
Lys 385	Tyr	Leu	Arg	Glu 390	Ala	Leu	Glu	Lys 395	Ser	Glu	Thr	Ser	Ser 400	Ala	Trp
Asn	Asn	Lys	Gln	Asn 405	Leu	Ser	Gln	Glu 410	Ile	Lys	Tyr	Ala	Leu 415	Lys	Thr
Ser	Trp	His	Ala	Ser 420	Val	Pro	Arg	Val 425	Glu	Ala	Lys	Arg	Tyr 430	Cys	Gln
Val	Tyr	Arg	Pro	Asp 435	Tyr	Ala	Arg	Ile 440	Ala	Lys	Cys	Val	Tyr 445	Lys	Leu

Pro Tyr Val Asn Asn Glu Lys Phe Leu Glu Leu Gly Lys Leu Asp Phe  
 450 455 460  
 Asn Ile Ile Gln Ser Ile His Gln Glu Glu Met Lys Asn Val Thr Ser  
 465 470 475 480  
 Trp Phe Arg Asp Ser Gly Leu Pro Leu Phe Thr Phe Ala Arg Glu Arg  
 485 490 495  
 Pro Leu Glu Phe Tyr Phe Leu Val Ala Ala Gly Thr Tyr Glu Pro Gln  
 500 505 510  
 Tyr Ala Lys Cys Arg Phe Leu Phe Thr Lys Val Ala Cys Leu Gln Thr  
 515 520 525  
 Val Leu Asp Asp Met Tyr Asp Thr Tyr Gly Thr Leu Asp Glu Leu Lys  
 530 535 540  
 Leu Phe Thr Glu Ala Val Arg Arg Trp Asp Leu Ser Phe Thr Glu Asn  
 545 550 555 560  
 Leu Pro Asp Tyr Met Lys Leu Cys Tyr Gln Ile Tyr Tyr Asp Ile Val  
 565 570 575  
 His Glu Val Ala Trp Glu Ala Glu Lys Glu Gln Gly Arg Glu Leu Val  
 580 585 590  
 Ser Phe Phe Arg Lys Gly Trp Glu Asp Tyr Leu Leu Gly Tyr Tyr Glu  
 595 600 605  
 Glu Ala Glu Trp Leu Ala Ala Glu Tyr Val Pro Thr Leu Asp Glu Tyr  
 610 615 620  
 Ile Lys Asn Gly Ile Thr Ser Ile Gly Gln Arg Ile Leu Leu Leu Ser  
 625 630 635 640  
 Gly Val Leu Ile Met Asp Gly Gln Leu Leu Ser Gln Glu Ala Leu Glu  
 645 650 655  
 Lys Val Asp Tyr Pro Gly Arg Arg Val Leu Thr Glu Leu Asn Ser Leu  
 660 665 670  
 Ile Ser Arg Leu Ala Asp Asp Thr Lys Thr Tyr Lys Ala Glu Lys Ala  
 675 680 685  
 Arg Gly Glu Leu Ala Ser Ser Ile Glu Cys Tyr Met Lys Asp His Pro  
 690 695 700  
 Glu Cys Thr Glu Glu Glu Ala Leu Asp His Ile Tyr Ser Ile Leu Glu  
 705 710 715 720  
 Pro Ala Val Lys Glu Leu Thr Arg Glu Phe Leu Lys Pro Asp Asp Val  
 725 730 735  
 Pro Phe Ala Cys Lys Lys Met Leu Phe Glu Glu Thr Arg Val Thr Met  
 740 745 750  
 Val Ile Phe Lys Asp Gly Asp Gly Phe Gly Val Ser Lys Leu Glu Val  
 755 760 765  
 Lys Asp His Ile Lys Glu Cys Leu Ile Glu Pro Leu Pro Leu  
 770 775 780

&lt;210&gt; 47

&lt;211&gt; 1865

&lt;212&gt; DNA

&lt;213&gt; Abies grandis

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1743)

&lt;223&gt; d-selinene synthase

&lt;400&gt; 47

atg gct gag att tct gaa tct tcc atc cct cga cgc aca ggg aat cat  
 Met Ala Glu Ile Ser Glu Ser Ser Ile Pro Arg Arg Thr Gly Asn His  
 1 5 10 15

cac gga aat gtg tgg gac gat gac ctc ata cac tct ctc aac tcg ccc His Gly Asn Val Trp Asp Asp Asp Leu Ile His Ser Leu Asn Ser Pro 20 25 30	96
tat ggg gca cct gca tat tat gag ctc ctt caa aag ctt att cag gag Tyr Gly Ala Pro Ala Tyr Tyr Glu Leu Leu Gln Lys Leu Ile Gln Glu 35 40 45	144
atc aag cat tta ctt ttg act gaa atg gaa atg gat gat ggc gat cat Ile Lys His Leu Leu Leu Thr Glu Met Glu Met Asp Asp Gly Asp His 50 55 60	192
gat tta atc aaa cgt ctt cag atc gtt gac act ttg gaa tgc ctg gga Asp Leu Ile Lys Arg Leu Gln Ile Val Asp Thr Leu Glu Cys Leu Gly 65 70 75 80	240
atc gat aga cat ttt gaa cac gaa ata caa aca gct gct tta gat tac Ile Asp Arg His Phe Glu His Glu Ile Gln Thr Ala Ala Leu Asp Tyr 85 90 95	288
gtt tac aga tgg tgg aac gaa aaa ggt atc ggg gag gga tca aga gat Val Tyr Arg Trp Trp Asn Glu Lys Gly Ile Gly Glu Gly Ser Arg Asp 100 105 110	336
tcc ttc agc aaa gat ctg aac gct acg gct tta gga ttt cgc gct ctc Ser Phe Ser Lys Asp Leu Asn Ala Thr Ala Leu Gly Phe Arg Ala Leu 115 120 125	384
cga ctg cat cga tat aac gta tcg tca ggt gtg ttg aag aat ttc aag Arg Leu His Arg Tyr Asn Val Ser Ser Gly Val Leu Lys Asn Phe Lys 130 135 140	432
gat gaa aac ggg aag ttc ttc tgc aac ttt act ggt gaa gaa gga aga Asp Glu Asn Gly Lys Phe Phe Cys Asn Phe Thr Gly Glu Glu Gly Arg 145 150 155 160	480
gga gat aaa caa gtg aga agc atg ttg tcg tta ctt cga gct tca gag Gly Asp Lys Gln Val Arg Ser Met Leu Ser Leu Leu Arg Ala Ser Glu 165 170 175	528
att tcg ttt ccc gga gaa aaa gtg atg gaa gag gcc aag gca ttc aca Ile Ser Phe Pro Gly Glu Lys Val Met Glu Glu Ala Lys Ala Phe Thr 180 185 190	576
aga gaa tat cta aac caa gtt tta gct gga cac ggg gat gtg act gac Arg Glu Tyr Leu Asn Gln Val Leu Ala Gly His Gly Asp Val Thr Asp 195 200 205	624
gtg gat caa agc ctt ttg aga gag gtg aag tac gca ttg gag ttt cca Val Asp Gln Ser Leu Leu Arg Glu Val Lys Tyr Ala Leu Glu Phe Pro 210 215 220	672
tgg cat tgc agt gtg ccg aga tgg gag gca agg agc ttt ctc gaa ata Trp His Cys Ser Val Pro Arg Trp Glu Ala Arg Ser Phe Leu Glu Ile 225 230 235 240	720

T02290"0222696



tat gga cac aac cat tcg tgg ctc aag tcg aat atc aac caa aaa atg Tyr Gly His Asn His Ser Trp Leu Lys Ser Asn Ile Asn Gln Lys Met 245 250 255	768
ttg aag tta gcc aaa ttg gac ttc aat att ctg caa tgc aaa cat cac Leu Lys Leu Ala Lys Leu Asp Phe Asn Ile Leu Gln Cys Lys His His 260 265 270	816
aag gag ata cag ttt att aca agg tgg tgg aga gac tcg ggt ata tcg Lys Glu Ile Gln Phe Ile Thr Arg Trp Trp Arg Asp Ser Gly Ile Ser 275 280 285	864
cag ctg aat ttc tat cga aag cga cac gtg gaa tat tat tct tgg gtt Gln Leu Asn Phe Tyr Arg Lys Arg His Val Glu Tyr Tyr Ser Trp Val 290 295 300	912
gtt atg tgc att ttt gag cca gag ttc tct gaa agt aga att gcc ttc Val Met Cys Ile Phe Glu Pro Glu Phe Ser Glu Ser Arg Ile Ala Phe 305 310 315 320	960
gcc aaa act gct atc ctg tgt act gtt cta gat gac ctc tat gat acg Ala Lys Thr Ala Ile Leu Cys Thr Val Leu Asp Asp Leu Tyr Asp Thr 325 330 335	1008
cac gca aca ttg cat gaa atc aaa atc atg aca gag gga gtg aga cga His Ala Thr Leu His Glu Ile Lys Ile Met Thr Glu Gly Val Arg Arg 340 345 350	1056
tgg gat ctt tcg ttg aca gat gac ctc cca gac tac att aaa att gca Trp Asp Leu Ser Leu Thr Asp Asp Leu Pro Asp Tyr Ile Lys Ile Ala 355 360 365	1104
ttc cag ttc ttc ttc aat aca gtg aat gaa ttg ata gtt gaa atc gtg Phe Gln Phe Phe Phe Asn Thr Val Asn Glu Leu Ile Val Glu Ile Val 370 375 380	1152
aaa cgg caa ggg cgg gat atg aca acc ata gtt aaa gat tgc tgg aag Lys Arg Gln Gly Arg Asp Met Thr Thr Ile Val Lys Asp Cys Trp Lys 385 390 395 400	1200
cga tac att gag tct tat ctg caa gaa gcg gaa tgg ata gca act gga Arg Tyr Ile Glu Ser Tyr Leu Gln Glu Ala Glu Trp Ile Ala Thr Gly 405 410 415	1248
cat att ccc act ttt aac gaa tac ata aag aac ggc atg gct agc tca His Ile Pro Thr Phe Asn Glu Tyr Ile Lys Asn Gly Met Ala Ser Ser 420 425 430	1296
ggg atg tgt att cta aat ttg aat cca ctt ctc ttg ttg gat aaa ctt Gly Met Cys Ile Leu Asn Leu Asn Pro Leu Leu Leu Leu Asp Lys Leu 435 440 445	1344
ctc ccc gac aac att ctg gag caa ata cat tct cca tcc aag atc ctg Leu Pro Asp Asn Ile Leu Glu Gln Ile His Ser Pro Ser Lys Ile Leu 450 455 460	1392
gac ctc tta gaa ttg acg ggc aga atc gcc gat gac tta aaa gat ttc	1440

Asp Leu Leu Glu Leu Thr Gly Arg Ile Ala Asp Asp Leu Lys Asp Phe  
 465 470 475 480  
 gag gac gag aag gaa cgc ggg gag atg gct tca tct tta cag tgt tat 1488  
 Glu Asp Glu Lys Glu Arg Gly Glu Met Ala Ser Ser Leu Gln Cys Tyr  
 485 490 495  
 atg aaa gaa aat cct gaa tct aca gtg gaa aat gct tta aat cac ata 1536  
 Met Lys Glu Asn Pro Glu Ser Thr Val Glu Asn Ala Leu Asn His Ile  
 500 505 510  
 aaa ggc atc ctt aat cgt tcc ctt gag gaa ttt aat tgg gag ttt atg 1584  
 Lys Gly Ile Leu Asn Arg Ser Leu Glu Glu Phe Asn Trp Glu Phe Met  
 515 520 525  
 aag cag gat agt gtc cca atg tgt tgc aag aaa ttc act ttc aat ata 1632  
 Lys Gln Asp Ser Val Pro Met Cys Cys Lys Lys Phe Thr Phe Asn Ile  
 530 535 540  
 ggt cga gga ctt caa ttc atc tac aaa tac aga gac ggc tta tac att 1680  
 Gly Arg Gly Leu Gln Phe Ile Tyr Lys Tyr Arg Asp Gly Leu Tyr Ile  
 545 550 555 560  
 tct gac aag gaa gta aag gac cag ata ttc aaa att cta gtc cac caa 1728  
 Ser Asp Lys Glu Val Lys Asp Gln Ile Phe Lys Ile Leu Val His Gln  
 565 570 575  
 gtt cca atg gag gaa tag tgatggtctt ggttgtagtt gtctattatg 1776  
 Val Pro Met Glu Glu  
 580  
 gtatatgca ttgacattta tgcttaaagg tgtttcttaa acgttttaggg cggaccgtta 1836  
 aataagttgg caataattaa tatctcgag 1865

<210> 48  
 <211> 581  
 <212> PRT  
 <213> Abies grandis

<400> 48  
 Met Ala Glu Ile Ser Glu Ser Ser Ile Pro Arg Arg Thr Gly Asn His  
 1 5 10 15  
 His Gly Asn Val Trp Asp Asp Asp Leu Ile His Ser Leu Asn Ser Pro  
 20 25 30  
 Tyr Gly Ala Pro Ala Tyr Tyr Glu Leu Leu Gln Lys Leu Ile Gln Glu  
 35 40 45  
 Ile Lys His Leu Leu Leu Thr Glu Met Glu Met Asp Asp Gly Asp His  
 50 55 60  
 Asp Leu Ile Lys Arg Leu Gln Ile Val Asp Thr Leu Glu Cys Leu Gly  
 65 70 75 80  
 Ile Asp Arg His Phe Glu His Glu Ile Gln Thr Ala Ala Leu Asp Tyr  
 85 90 95  
 Val Tyr Arg Trp Trp Asn Glu Lys Gly Ile Gly Glu Gly Ser Arg Asp  
 100 105 110  
 Ser Phe Ser Lys Asp Leu Asn Ala Thr Ala Leu Gly Phe Arg Ala Leu  
 115 120 125  
 Arg Leu His Arg Tyr Asn Val Ser Ser Gly Val Leu Lys Asn Phe Lys

[illegible]

<211> 1785

<213> Abies grandis

<221> CDS

<222> (4) ... (1782)

<223> gamma-humulene synthase

<400> 49

tcc atg gct cag att tct gaa tct gta tca ccc tct acc gat ttg aag 48  
Met Ala Gln Ile Ser Glu Ser Val Ser Pro Ser Thr Asp Leu Lys  
1 5 10 15

agc acc gaa tct tcc att acc tct aat cga cat gga aat atg tgg gag      96  
Ser Thr Glu Ser Ser Ile Thr Ser Asn Arg His Gly Asn Met Trp Glu  
                20                       25                              30

gac gat cgc ata cag tct ctc aac tca cct tat ggg gca oct gca tat 144  
Asp Asp Arg Ile Gln Ser Leu Asn Ser Pro Tyr Gly Ala Pro Ala Tyr  
35 40 45

caa gaa cgc agc gaa aag ctt att gaa gag atc aaa ctt tta ttt ttg 192  
Gln Glu Arg Ser Glu Lys Leu Ile Glu Glu Ile Lys Leu Leu Phe Leu  
50 55 60

```

agt gac atg gac gat agc tgc aat gat agc gat cgt gat tta atc aaa      240
Ser Asp Met Asp Asp Ser Cys Asn Asp Ser Asp Arg Asp Leu Ile Lys
      65              70              75

```

cgt ctt gag atc gtt gat act gtc gag tgt ctg gga att gat cga cat 288  
Arg Leu Glu Ile Val Asp Thr Val Glu Cys Leu Gly Ile Asp Arg His  
80 85 90 95

ttt caa cct gag ata aaa tta gct ctg gat tac gtt tac aga tgt tgg 336  
Phe Gln Pro Glu Ile Lys Leu Ala Leu Asp Tyr Val Tyr Arg Cys Trp  
100 105 110

aac gaa aga ggc atc gga gag gga tca aga gat tcc ctc aag aaa gat 384  
Asn Glu Arg Gly Ile Gly Glu Gly Ser Arg Asp Ser Leu Lys Lys Asp  
115 120 125

ctg aac gct aca gct ttg gga ttc cgg gct ctc cga ctc cat cga tat 432  
Leu Asn Ala Thr Ala Leu Gly Phe Arg Ala Leu Arg Leu His Arg Tyr  
130 135 140

aac gta tcc tca ggt gtc ttg gag aat ttc aga gat gat aac ggg cag 480  
Asn Val Ser Ser Gly Val Leu Glu Asn Phe Arg Asp Asp Asn Gly Gln  
145 150 155

ttc ttc tgc ggt tct aca gtt gaa gaa gaa gga gca gaa gca tat aat 528  
Phe Phe Cys Gly Ser Thr Val Glu Glu Glu Gly Ala Glu Ala Tyr Asn  
160 165 170 175

aaa cac gta aga tgc atg ctg tca tta tcg cga gct tca aac att tta 576

Lys	His	Val	Arg	Cys	Met	Leu	Ser	Leu	Ser	Arg	Ala	Ser	Asn	Ile	Leu	
				180					185					190		
ttt	ccg	ggc	gaa	aaa	gtg	atg	gaa	gag	gcg	aag	gca	ttc	aca	aca	aat	624
Phe	Pro	Gly	Glu	Lys	Val	Met	Glu	Glu	Ala	Lys	Ala	Phe	Thr	Thr	Asn	
				195					200					205		
tat	cta	aag	aaa	gtt	tta	gca	gga	cgg	gag	gct	acc	cac	gtc	gat	gaa	672
Tyr	Leu	Lys	Lys	Val	Leu	Ala	Gly	Arg	Glu	Ala	Thr	His	Val	Asp	Glu	
				210					215					220		
agc	ctt	ttg	gga	gag	gtg	aag	tac	gca	ttg	gag	ttt	cca	tgg	cat	tgc	720
Ser	Leu	Leu	Gly	Glu	Val	Lys	Tyr	Ala	Leu	Glu	Phe	Pro	Trp	His	Cys	
				225					230					235		
agt	gtg	cag	aga	tgg	gag	gca	agg	agc	ttt	atc	gaa	ata	ttt	gga	caa	768
Ser	Val	Gln	Arg	Trp	Glu	Ala	Arg	Ser	Phe	Ile	Glu	Ile	Phe	Gly	Gln	
				240					245					250		
att	gat	tca	gag	ctt	aag	tcg	aat	ttg	agc	aaa	aaa	atg	tta	gag	ttg	816
Ile	Asp	Ser	Glu	Leu	Lys	Ser	Asn	Leu	Ser	Lys	Lys	Met	Leu	Glu	Leu	
				260					265					270		
gcg	aaa	ttg	gac	ttc	aat	att	ctg	caa	tgc	aca	cat	cag	aaa	gaa	ctg	864
Ala	Lys	Leu	Asp	Phe	Asn	Ile	Leu	Gln	Cys	Thr	His	Gln	Lys	Glu	Leu	
				275					280					285		
cag	att	atc	tca	agg	tgg	ttc	gca	gac	tca	agt	ata	gca	tcc	ctg	aat	912
Gln	Ile	Ile	Ser	Arg	Trp	Phe	Ala	Asp	Ser	Ser	Ile	Ala	Ser	Leu	Asn	
				290					295					300		
ttc	tat	cgg	aaa	tgt	tac	gtc	gaa	ttt	tac	ttt	tgg	atg	gct	gca	gcc	960
Phe	Tyr	Arg	Lys	Cys	Tyr	Val	Glu	Phe	Tyr	Phe	Trp	Met	Ala	Ala	Ala	
				305					310					315		
atc	tcc	gag	ccg	gag	ttt	tct	gga	agc	aga	gtt	gcc	ttc	aca	aaa	att	1008
Ile	Ser	Glu	Pro	Glu	Phe	Ser	Gly	Ser	Arg	Val	Ala	Phe	Thr	Lys	Ile	
				320					325					330		
gct	ata	ctg	atg	aca	atg	cta	gat	gac	ctg	tac	gat	act	cac	gga	acc	1056
Ala	Ile	Leu	Met	Thr	Met	Leu	Asp	Asp	Leu	Tyr	Asp	Thr	His	Gly	Thr	
				340					345					350		
ttg	gac	caa	ctc	aaa	atc	ttt	aca	gag	gga	gtg	aga	cga	tgg	gat	gtt	1104
Leu	Asp	Gln	Leu	Lys	Ile	Phe	Thr	Glu	Gly	Val	Arg	Arg	Trp	Asp	Val	
				355					360					365		
tcg	ttg	gta	gag	ggc	ctc	cca	gac	ttc	atg	aaa	att	gca	ttc	gag	ttc	1152
Ser	Leu	Val	Glu	Gly	Leu	Pro	Asp	Phe	Met	Lys	Ile	Ala	Phe	Glu	Phe	
				370					375					380		
tgg	tta	aag	aca	tct	aat	gaa	ttg	att	gct	gaa	gct	gtt	aaa	gcg	caa	1200
Trp	Leu	Lys	Thr	Ser	Asn	Glu	Leu	Ile	Ala	Glu	Ala	Val	Lys	Ala	Gln	
				385					390					395		
ggg	caa	gat	atg	gcg	gcc	tac	ata	aga	aaa	aat	gca	tgg	gag	cga	tac	

400	405							410							415							
ctt gaa gct tat ctg caa gat gcg gaa tgg ata gcc act gga cat gtc																						1296
Leu Glu Ala Tyr Leu Gln Asp Ala Glu Trp Ile Ala Thr Gly His Val																						
	420							425							430							
ccc acc ttt gat gag tac ttg aat aat ggc aca cca aac act ggg atg																						1344
Pro Thr Phe Asp Glu Tyr Leu Asn Asn Gly Thr Pro Asn Thr Gly Met																						
	435							440							445							
tgt gta ttg aat ttg att ccg ctt ctg tta atg ggt gaa cat tta cca																						1392
Cys Val Leu Asn Leu Ile Pro Leu Leu Met Gly Glu His Leu Pro																						
	450							455							460							
atc gac att ctg gag caa ata ttc ttg ccc tcc agg ttc cac cat ctc																						1440
Ile Asp Ile Leu Glu Gln Ile Phe Leu Pro Ser Arg Phe His His Leu																						
	465							470							475							
att gaa ttg gct tcc agg ctc gtc gat gac gcg aga gat ttc cag gcg																						1488
Ile Glu Leu Ala Ser Arg Leu Val Asp Asp Ala Arg Asp Phe Gln Ala																						
	480							485							490							495
gag aag gat cat ggg gat tta tcg tgt att gag tgt tat tta aaa gat																						1536
Glu Lys Asp His Gly Asp Leu Ser Cys Ile Glu Cys Tyr Leu Lys Asp																						
	500							505							510							
cat cct gag tct aca gta gaa gat gct tta aat cat gtt aat ggc ctc																						1584
His Pro Glu Ser Thr Val Glu Asp Ala Leu Asn His Val Asn Gly Leu																						
	515							520							525							
ctt ggc aat tgc ctt ctg gaa atg aat tgg aag ttc tta aag aag cag																						1632
Leu Gly Asn Cys Leu Leu Glu Met Asn Trp Lys Phe Leu Lys Lys Gln																						
	530							535							540							
gac agt gtg cca ctc tcg tgt aag aag tac agc ttc cat gta ttg gca																						1680
Asp Ser Val Pro Leu Ser Cys Lys Lys Tyr Ser Phe His Val Leu Ala																						
	545							550							555							
cga agc atc caa ttc atg tac aat caa ggc gat ggc ttc tcc att tcg																						1728
Arg Ser Ile Gln Phe Met Tyr Asn Gln Gly Asp Gly Phe Ser Ile Ser																						
	560							565							570							575
aac aaa gtg atc aag gat caa gtg cag aaa gtt ctt att gtc ccc gtg																						1776
Asn Lys Val Ile Lys Asp Gln Val Gln Lys Val Leu Ile Val Pro Val																						
	580							585							590							
cct att tga															1785							
Pro Ile																						
<210> 50																						
<211> 593																						
<212> PRT																						
<213> Abies grandis																						
<400> 50																						
Met Ala Gln Ile Ser Glu Ser Val Ser Pro Ser Thr Asp Leu Lys Ser																						
1 5 10 15																						

Thr	Glu	Ser	Ser	Ile	Thr	Ser	Asn	Arg	His	Gly	Asn	Met	Trp	Glu	Asp
			20					25					30		
Asp	Arg	Ile	Gln	Ser	Leu	Asn	Ser	Pro	Tyr	Gly	Ala	Pro	Ala	Tyr	Gln
		35				40					45				
Glu	Arg	Ser	Glu	Lys	Leu	Ile	Glu	Glu	Ile	Lys	Leu	Leu	Phe	Leu	Ser
	50				55					60					
Asp	Met	Asp	Asp	Ser	Cys	Asn	Asp	Ser	Asp	Arg	Asp	Leu	Ile	Lys	Arg
65				70					75					80	
Leu	Glu	Ile	Val	Asp	Thr	Val	Glu	Cys	Leu	Gly	Ile	Asp	Arg	His	Phe
			85					90						95	
Gln	Pro	Glu	Ile	Lys	Leu	Ala	Leu	Asp	Tyr	Val	Tyr	Arg	Cys	Trp	Asn
		100						105					110		
Glu	Arg	Gly	Ile	Gly	Glu	Gly	Ser	Arg	Asp	Ser	Leu	Lys	Lys	Asp	Leu
		115					120					125			
Asn	Ala	Thr	Ala	Leu	Gly	Phe	Arg	Ala	Leu	Arg	Leu	His	Arg	Tyr	Asn
	130					135					140				
Val	Ser	Ser	Gly	Val	Leu	Glu	Asn	Phe	Arg	Asp	Asp	Asn	Gly	Gln	Phe
145				150						155				160	
Phe	Cys	Gly	Ser	Thr	Val	Glu	Glu	Glu	Gly	Ala	Glu	Ala	Tyr	Asn	Lys
			165						170					175	
His	Val	Arg	Cys	Met	Leu	Ser	Leu	Ser	Arg	Ala	Ser	Asn	Ile	Leu	Phe
		180						185					190		
Pro	Gly	Glu	Lys	Val	Met	Glu	Glu	Ala	Lys	Ala	Phe	Thr	Thr	Asn	Tyr
		195				200					205				
Leu	Lys	Lys	Val	Leu	Ala	Gly	Arg	Glu	Ala	Thr	His	Val	Asp	Glu	Ser
	210					215					220				
Leu	Leu	Gly	Glu	Val	Lys	Tyr	Ala	Leu	Glu	Phe	Pro	Trp	His	Cys	Ser
225				230						235				240	
Val	Gln	Arg	Trp	Glu	Ala	Arg	Ser	Phe	Ile	Glu	Ile	Phe	Gly	Gln	Ile
			245						250					255	
Asp	Ser	Glu	Leu	Lys	Ser	Asn	Leu	Ser	Lys	Lys	Met	Leu	Glu	Leu	Ala
		260						265				270			
Lys	Leu	Asp	Phe	Asn	Ile	Leu	Gln	Cys	Thr	His	Gln	Lys	Glu	Leu	Gln
		275					280					285			
Ile	Ile	Ser	Arg	Trp	Phe	Ala	Asp	Ser	Ser	Ile	Ala	Ser	Leu	Asn	Phe
	290				295						300				
Tyr	Arg	Lys	Cys	Tyr	Val	Glu	Phe	Tyr	Phe	Trp	Met	Ala	Ala	Ala	Ile
305				310						315				320	
Ser	Glu	Pro	Glu	Phe	Ser	Gly	Ser	Arg	Val	Ala	Phe	Thr	Lys	Ile	Ala
			325						330					335	
Ile	Leu	Met	Thr	Met	Leu	Asp	Asp	Leu	Tyr	Asp	Thr	His	Gly	Thr	Leu
		340						345					350		
Asp	Gln	Leu	Lys	Ile	Phe	Thr	Glu	Gly	Val	Arg	Arg	Trp	Asp	Val	Ser
		355					360					365			
Leu	Val	Glu	Gly												

```
<210> 51
<211> 2024
<212> DNA
<213> Lycopersicon esculentum
```

<400>	51																	52
aaaaaaagcc aaacottaga acaaacaagc a	atg gct gct tct tct gct gat																	
	Met Ala Ala Ser Ser Ala Asp																	
	1															5		
aag tgt cgc ccc ttg gct aat ttt cac cca tct gtt tgg gga tat cat																	100	
Lys Cys Arg Pro Leu Ala Asn Phe His Pro Ser Val Trp Gly Tyr His																		
	10															20		
ttc ctt tct tat act cat gaa att act aat caa gaa aaa gtt gaa gtt																	148	
Phe Leu Ser Tyr Thr His Glu Ile Thr Asn Gln Glu Lys Val Glu Val																		
	25															35		
gat gag tac aaa gag aca att aga aaa atg ctg gtg gaa act tgc gac																	196	
Asp Glu Tyr Lys Glu Thr Ile Arg Lys Met Leu Val Glu Thr Cys Asp																		
	40															55		
aat agc act caa aag ctt gtg ttg ata gac gcg atg caa cga ttg gga																	244	
Asn Ser Thr Gln Lys Leu Val Leu Ile Asp Ala Met Gln Arg Leu Gly																		
	60															70		
gtg gct tat cat ttc gat aat gaa att gaa aca tcc att caa aac att																	292	
Val Ala Tyr His Phe Asp Asn Glu Ile Glu Thr Ser Ile Gln Asn Ile																		
	75															85		
ttt gat gca tcg tcc aaa cag aat gat aat gac aac aac ctt tac gtt																	340	
Phe Asp Ala Ser Ser Lys Gln Asn Asp Asn Asp Asn Asn Leu Tyr Val																		
	90															100		



gtg tct ctt cgt ttt cga ctt gtg agg caa caa ggc cat tac atg tct	388
Val Ser Leu Arg Phe Arg Leu Val Arg Gln Gln Gly His Tyr Met Ser	
105 110 115	
tca gat gtg ttc aag caa ttc acc aac caa gat ggg aaa ttc aag gaa	436
Ser Asp Val Phe Lys Gln Phe Thr Asn Gln Asp Gly Lys Phe Lys Glu	
120 125 130 135	
aca ctt act aat gat gtc caa gga tta ttg agt ttg tat gaa gca tca	484
Thr Leu Thr Asn Asp Val Gln Gly Leu Leu Ser Leu Tyr Glu Ala Ser	
140 145 150	
cat ctg aga gtg cgt aat gag gag att ctt gaa gaa gct ctt aca ttt	532
His Leu Arg Val Arg Asn Glu Glu Ile Leu Glu Glu Ala Leu Thr Phe	
155 160 165	
acc acc act cat ctc gag tct att gtc tcc aac ttg agc aat aat aat	580
Thr Thr Thr His Leu Glu Ser Ile Val Ser Asn Leu Ser Asn Asn Asn	
170 175 180	
aac tct ctt aag gtt gaa gtt ggt gaa gcc tta act cag cct att cgc	628
Asn Ser Leu Lys Val Glu Val Gly Glu Ala Leu Thr Gln Pro Ile Arg	
185 190 195	
atg act tta cca agg atg gga gct aga aaa tac ata tcc att tac gaa	676
Met Thr Leu Pro Arg Met Gly Ala Arg Lys Tyr Ile Ser Ile Tyr Glu	
200 205 210 215	
aac aat gat gca cac cac cat ttg ctt ttg aaa ttt gct aaa ttg gat	724
Asn Asn Asp Ala His His His Leu Leu Leu Lys Phe Ala Lys Leu Asp	
220 225 230	
ttt aac atg ctg caa aag ttt cac caa aga gag ctt agt gat ctt aca	772
Phe Asn Met Leu Gln Lys Phe His Gln Arg Glu Leu Ser Asp Leu Thr	
235 240 245	
agg tgg tgg aaa gat ttg gat ttt gca aat aaa tat cca tat gca aga	820
Arg Trp Trp Lys Asp Leu Asp Phe Ala Asn Lys Tyr Pro Tyr Ala Arg	
250 255 260	
gac agg ttg gtt gag tgt tac ttc tgg ata tta gga gtg tat ttt gag	868
Asp Arg Leu Val Glu Cys Tyr Phe Trp Ile Leu Gly Val Tyr Phe Glu	
265 270 275	
cca aaa tat agt cgt gcg aga aaa atg atg aca aaa gta ctc aac ctg	916
Pro Lys Tyr Ser Arg Ala Arg Lys Met Met Thr Lys Val Leu Asn Leu	
280 285 290 295	
acc tcc att att gac gac act ttt gat gct tat gca acc ttt gac gaa	964
Thr Ser Ile Ile Asp Asp Thr Phe Asp Ala Tyr Ala Thr Phe Asp Glu	
300 305 310	
ctt gtg act ttc aat gat gca atc cag aga tgg gat gct aat gca att	1012
Leu Val Thr Phe Asn Asp Ala Ile Gln Arg Trp Asp Ala Asn Ala Ile	
315 320 325	
gat tca ata caa cca tat atg aga cct gct tat caa gct ctt cta gac	1060

F00000-000000

Asp	Ser	Ile	Gln	Pro	Tyr	Met	Arg	Pro	Ala	Tyr	Gln	Ala	Leu	Leu	Asp	
		330					335					340				
att	tac	agt	gaa	atg	gaa	caa	gtg	ttg	tcc	aaa	gaa	ggt	aaa	ctg	gac	1108
Ile	Tyr	Ser	Glu	Met	Glu	Gln	Val	Leu	Ser	Lys	Glu	Gly	Lys	Leu	Asp	
		345				350					355					
cgt	gta	tac	tat	gca	aaa	aat	gag	atg	aaa	aag	ttg	gtg	aga	gcc	tat	1156
Arg	Val	Tyr	Tyr	Ala	Lys	Asn	Glu	Met	Lys	Lys	Leu	Val	Arg	Ala	Tyr	
					365					370					375	
ttt	aag	gaa	acc	caa	tgg	ttg	aat	gat	tgt	gac	cat	att	cca	aaa	tat	1204
Phe	Lys	Glu	Thr	Gln	Trp	Leu	Asn	Asp	Cys	Asp	His	Ile	Pro	Lys	Tyr	
				380					385					390		
gag	gaa	caa	gtg	gag	aat	gca	atc	gta	agt	gct	ggc	tat	atg	atg	ata	1252
Glu	Glu	Gln	Val	Glu	Asn	Ala	Ile	Val	Ser	Ala	Gly	Tyr	Met	Met	Ile	
			395					400					405			
tca	aca	act	tgc	ttg	gtc	ggt	ata	gaa	gaa	ttt	ata	tcc	cac	gag	act	1300
Ser	Thr	Thr	Cys	Leu	Val	Gly	Ile	Glu	Glu	Phe	Ile	Ser	His	Glu	Thr	
		410					415					420				
ttt	gaa	tgg	ttg	atg	aat	gag	tct	gtg	att	gtt	cga	gct	tcc	gca	ttg	1348
Phe	Glu	Trp	Leu	Met	Asn	Glu	Ser	Val	Ile	Val	Arg	Ala	Ser	Ala	Leu	
		425				430					435					
att	gcc	aga	gca	atg	aac	gat	att	gtt	gga	cat	gaa	gat	gaa	caa	gaa	1396
Ile	Ala	Arg	Ala	Met	Asn	Asp	Ile	Val	Gly	His	Glu	Asp	Glu	Gln	Glu	
					445					450					455	
aga	gga	cat	gta	gct	tca	ctt	att	gaa	tgt	tac	atg	aaa	gat	tat	gga	1444
Arg	Gly	His	Val	Ala	Ser	Leu	Ile	Glu	Cys	Tyr	Met	Lys	Asp	Tyr	Gly	
			460						465					470		
gct	tca	aag	caa	gag	act	tac	att	aag	ttc	ctg	aaa	gag	gtc	acc	aat	1492
Ala	Ser	Lys	Gln	Glu	Thr	Tyr	Ile	Lys	Phe	Leu	Lys	Glu	Val	Thr	Asn	
			475					480					485			
gca	tgg	aag	gac	ata	aac	aaa	caa	ttc	tcc	cgt	cca	act	gaa	gta	cca	1540
Ala	Trp	Lys	Asp	Ile	Asn	Lys	Gln	Phe	Ser	Arg	Pro	Thr	Glu	Val	Pro	
		490					495					500				
atg	ttt	gtc	ctt	gaa	cga	gtt	cta	aat	ttg	aca	cgt	gtg	gct	gac	acg	1588
Met	Phe	Val	Leu	Glu	Arg	Val	Leu	Asn	Leu	Thr	Arg	Val	Ala	Asp	Thr	
		505				510					515					
tta	tat	aag	gag	aaa	gat	aca	tat	tca	acc	gcc	aaa	gga	aaa	ctt	aaa	1636
Leu	Tyr	Lys	Glu	Lys	Asp	Thr	Tyr	Ser	Thr	Ala	Lys	Gly	Lys	Leu	Lys	
					525					530					535	
aac	atg	att	aat	cca	ata	cta	att	gaa	tct	gtc	aaa	ata	taa			1678
Asn	Met	Ile	Asn	Pro	Ile	Leu	Ile	Glu	Ser	Val	Lys	Ile				

1858  
1918  
1978  
2024

<400>	52															
Met	Ala	Ala	Ser	Ser	Ala	Asp	Lys	Cys	Arg	Pro	Leu	Ala	Asn	Phe	His	
1				5					10					15		
Pro	Ser	Val	Trp	Gly	Tyr	His	Phe	Leu	Ser	Tyr	Thr	His	Glu	Ile	Thr	
			20					25					30			
Asn	Gln	Glu	Lys	Val	Glu	Val	Asp	Glu	Tyr	Lys	Glu	Thr	Ile	Arg	Lys	
		35					40					45				
Met	Leu	Val	Glu	Thr	Cys	Asp	Asn	Ser	Thr	Gln	Lys	Leu	Val	Leu	Ile	
50						55					60					
Asp	Ala	Met	Gln	Arg	Leu	Gly	Val	Ala	Tyr	His	Phe	Asp	Asn	Glu	Ile	
65				70						75					80	
Glu	Thr	Ser	Ile	Gln	Asn	Ile	Phe	Asp	Ala	Ser	Ser	Lys	Gln	Asn	Asp	
				85					90					95		
Asn	Asp	Asn	Asn	Leu	Tyr	Val	Val	Ser	Leu	Arg	Phe	Arg	Leu	Val	Arg	
			100					105					110			
Gln	Gln	Gly	His	Tyr	Met	Ser	Ser	Asp	Val	Phe	Lys	Gln	Phe	Thr	Asn	
		115					120					125				
Gln	Asp	Gly	Lys	Phe	Lys	Glu	Thr	Leu	Thr	Asn	Asp	Val	Gln	Gly	Leu	
130						135					140					
Leu	Ser	Leu	Tyr	Glu	Ala	Ser	His	Leu	Arg	Val	Arg	Asn	Glu	Glu	Ile	
145				150						155					160	
Leu	Glu	Glu	Ala	Leu	Thr	Phe	Thr	Thr	Thr	His	Leu	Glu	Ser	Ile	Val	
				165					170					175		
Ser	Asn	Leu	Ser	Asn	Asn	Asn	Asn	Ser	Leu	Lys	Val	Glu	Val	Gly	Glu	
			180					185					190			
Ala	Leu	Thr	Gln	Pro	Ile	Arg	Met	Thr	Leu	Pro	Arg	Met	Gly	Ala	Arg	
		195					200					205				
Lys	Tyr	Ile	Ser	Ile	Tyr	Glu	Asn	Asn	Asp	Ala	His	His	His	Leu	Leu	
210						215					220					
Leu	Lys	Phe	Ala	Lys	Leu	Asp	Phe	Asn	Met	Leu	Gln	Lys	Phe	His	Gln	
225				230						235					240	
Arg	Glu	Leu	Ser	Asp	Leu	Thr	Arg	Trp	Trp	Lys	Asp	Leu	Asp	Phe	Ala	
				245					250					255		
Asn	Lys	Tyr	Pro	Tyr	Ala	Arg	Asp	Arg	Leu	Val	Glu	Cys	Tyr	Phe	Trp	
			260				265						270			
Ile	Leu	Gly	Val	Tyr	Phe	Glu	Pro	Lys	Tyr	Ser	Arg	Ala	Arg	Lys	Met	
		275					280					285				
Met	Thr	Lys	Val	Leu	Asn	Leu	Thr	Ser	Ile	Ile	Asp	Asp	Thr	Phe	Asp	
290						295					300					
Ala	Tyr	Ala	Thr	Phe	Asp	Glu	Leu	Val	Thr	Phe	Asn	Asp	Ala	Ile	Gln	
305				310						315					320	
Arg	Trp	Asp	Ala	Asn	Ala	Ile	Asp	Ser	Ile	Gln	Pro	Tyr	Met	Arg	Pro	

Lys Lys Leu Val Arg Ala Tyr Phe Lys Glu Thr Gln Trp Leu Asn Asp  
 370 375 380  
 Cys Asp His Ile Pro Lys Tyr Glu Glu Gln Val Glu Asn Ala Ile Val  
 385 390 395 400  
 Ser Ala Gly Tyr Met Met Ile Ser Thr Thr Cys Leu Val Gly Ile Glu  
 405 410 415  
 Glu Phe Ile Ser His Glu Thr Phe Glu Trp Leu Met Asn Glu Ser Val  
 420 425 430  
 Ile Val Arg Ala Ser Ala Leu Ile Ala Arg Ala Met Asn Asp Ile Val  
 435 440 445  
 Gly His Glu Asp Glu Gln Glu Arg Gly His Val Ala Ser Leu Ile Glu  
 450 455 460  
 Cys Tyr Met Lys Asp Tyr Gly Ala Ser Lys Gln Glu Thr Tyr Ile Lys  
 465 470 475 480  
 Phe Leu Lys Glu Val Thr Asn Ala Trp Lys Asp Ile Asn Lys Gln Phe  
 485 490 495  
 Ser Arg Pro Thr Glu Val Pro Met Phe Val Leu Glu Arg Val Leu Asn  
 500 505 510  
 Leu Thr Arg Val Ala Asp Thr Leu Tyr Lys Glu Lys Asp Thr Tyr Ser  
 515 520 525  
 Thr Ala Lys Gly Lys Leu Lys Asn Met Ile Asn Pro Ile Leu Ile Glu  
 530 535 540  
 Ser Val Lys Ile  
 545

<210> 53  
 <211> 1912  
 <212> DNA  
 <213> *Salvia officinalis*  
  
 <220>  
 <221> CDS  
 <222> (26)...(1795)  
 <223> (+)-sabinene synthase

<400> 53  
 agcaatatta caactaacaa taaaa atg tct tcc att agc ata aac ata gct 52  
 Met Ser Ser Ile Ser Ile Asn Ile Ala  
 1 5  
  
 atg cca ctg aat tcc ctc cac aac ttt gag agg aaa cct tca aaa gca 100  
 Met Pro Leu Asn Ser Leu His Asn Phe Glu Arg Lys Pro Ser Lys Ala  
 10 15 20 25  
  
 tgg tct acc tct tgc act gca ccc gca gct cgc ctc cgg gca tct tcc 148  
 Trp Ser Thr Ser Cys Thr Ala Pro Ala Ala Arg Leu Arg Ala Ser Ser  
 30 35 40  
  
 tcc tta caa caa gaa aaa cct cac caa atc cga cgc tct ggg gat tac 196  
 Ser Leu Gln Gln Glu Lys Pro His Gln Ile Arg Arg Ser Gly Asp Tyr  
 45 50 55  
  
 caa ccc tct ctt tgg gat ttc aat tac ata cag tct ctc aac act ccg 244  
 Gln Pro Ser Leu Trp Asp Phe Asn Tyr Ile Gln Ser Leu Asn Thr Pro  
 60 65 70  
  
 tat aag gag cag aga cac ttt aat agg caa gca gag ttg att atg caa 292

Tyr	Lys	Glu	Gln	Arg	His	Phe	Asn	Arg	Gln	Ala	Glu	Leu	Ile	Met	Gln	
75						80					85					
gtg	agg	atg	ttg	ctc	aag	gta	aag	atg	gag	gca	att	caa	cag	ttg	gag	340
Val	Arg	Met	Leu	Leu	Lys	Val	Lys	Met	Glu	Ala	Ile	Gln	Gln	Leu	Glu	
90					95					100					105	
ttg	att	gat	gac	ttg	caa	tac	ctg	gga	ctg	tct	tat	ttc	ttt	caa	gat	388
Leu	Ile	Asp	Asp	Leu	Gln	Tyr	Leu	Gly	Leu	Ser	Tyr	Phe	Phe	Gln	Asp	
				110					115					120		
gag	att	aaa	caa	atc	tta	agt	tct	ata	cac	aat	gag	ccc	aga	tat	ttc	436
Glu	Ile	Lys	Gln	Ile	Leu	Ser	Ser	Ile	His	Asn	Glu	Pro	Arg	Tyr	Phe	
			125					130					135			
cac	aat	aat	gat	ttg	tat	ttc	aca	gct	ctt	gga	ttc	aga	atc	ctc	aga	484
His	Asn	Asn	Asp	Leu	Tyr	Phe	Thr	Ala	Leu	Gly	Phe	Arg	Ile	Leu	Arg	
			140				145					150				
caa	cat	ggt	ttt	aat	gtt	tcc	gaa	gat	gta	ttt	gat	tgt	ttc	aaa	att	532
Gln	His	Gly	Phe	Asn	Val	Ser	Glu	Asp	Val	Phe	Asp	Cys	Phe	Lys	Ile	
			155			160					165					
gag	aag	tgc	agt	gat	ttc	aat	gca	aac	ctt	gct	caa	gat	acg	aag	gga	580
Glu	Lys	Cys	Ser	Asp	Phe	Asn	Ala	Asn	Leu	Ala	Gln	Asp	Thr	Lys	Gly	
170					175					180					185	
atg	tta	caa	ctt	tat	gaa	gca	tct	ttc	ctt	ttg	aga	gaa	ggt	gaa	gat	628
Met	Leu	Gln	Leu	Tyr	Glu	Ala	Ser	Phe	Leu	Leu	Arg	Glu	Gly	Glu	Asp	
				190					195					200		
aca	ttg	gag	cta	gca	aga	cga	ttt	tcc	acc	aga	tct	cta	cga	gaa	aaa	676
Thr	Leu	Glu	Leu	Ala	Arg	Arg	Phe	Ser	Thr	Arg	Ser	Leu	Arg	Glu	Lys	
			205					210					215			
ttt	gat	gaa	ggt	ggt	gat	gaa	att	gat	gaa	gat	cta	tca	tcg	tggt	att	724
Phe	Asp	Glu	Gly	Gly	Asp	Glu	Ile	Asp	Glu	Asp	Leu	Ser	Ser	Trp	Ile	
		220				225					230					
cgc	cat	tcc	ttg	gat	ctt	cct	ctt	cat	tgg	agg	gtc	caa	gga	tta	gag	772
Arg	His	Ser	Leu	Asp	Leu	Pro	Leu	His	Trp	Arg	Val	Gln	Gly	Leu	Glu	
			235			240					245					
gca	aga	tgg	ttc	tta	gat	gct	tat	gcg	agg	agg	ccg	gac	atg	aat	cca	820
Ala	Arg	Trp	Phe	Leu	Asp	Ala	Tyr	Ala	Arg	Arg	Pro	Asp	Met	Asn	Pro	
250					255				260						265	
ctt	att	ttc	aaa	ctc	gcc	aaa	ctc	aac	ttc	aat	att	gtt	cag	gca	aca	868
Leu	Ile	Phe	Lys	Leu	Ala	Lys	Leu	Asn	Phe	Asn	Ile	Val	Gln	Ala	Thr	
				270					275					280		
tat	caa	gaa	gaa	ctg	aaa	gat	atc	tca	agg	tgg	tgg	aat	agt	tcg	tgc	916
Tyr	Gln	Glu	Glu	Leu	Lys	Asp	Ile	Ser	Arg	Trp	Trp	Asn	Ser	Ser	Cys	
			285					290					295			
ctt	gct	gag	aaa	ctc	cca	ttt	gtg	aga	gat	agg	att	gtg	gaa	tgc	ttc	964
Leu	Ala	Glu	Lys	Leu	Pro	Phe	Val	Arg	Asp	Arg	Ile	Val	Glu	Cys	Phe	

T02290"0222222222

300	305	310	
ttt tgg gcc atc gcg gct	ttt gag cct cac caa	tat agt tat cag aga	1012
Phe Trp Ala Ile Ala Ala	Phe Glu Pro His Gln	Tyr Ser Tyr Gln Arg	
315	320	325	
aaa atg gcc gcc gtt att	att act ttc ata aca	att atc gat gat gtt	1060
Lys Met Ala Ala Val Ile	Ile Thr Phe Ile Thr	Ile Ile Asp Asp Val	
330	335	340	345
tat gat gtg tat gga aca	ata gaa gaa cta gaa	cta tta aca gat atg	1108
Tyr Asp Val Tyr Gly Thr	Ile Glu Glu Leu Glu	Leu Leu Thr Asp Met	
350	355	360	
att cgc aga tgg gat aat	aaa tca ata agc caa	ctt cca tat tat atg	1156
Ile Arg Arg Trp Asp Asn	Lys Ser Ile Ser Gln	Leu Pro Tyr Tyr Met	
365	370	375	
caa gtg tgc tat ttg gca	cta tac aac ttc gtt	tct gag cgg gct tac	1204
Gln Val Cys Tyr Leu Ala	Leu Tyr Asn Phe Val	Ser Glu Arg Ala Tyr	
380	385	390	
gat att cta aaa gat caa	cat ttc aac agc atc	cca tat tta cag aga	1252
Asp Ile Leu Lys Asp Gln	His Phe Asn Ser Ile	Pro Tyr Leu Gln Arg	
395	400	405	
tcg tgg gta agt ttg gtt	gaa gga tat ctt aag	gag gca tac tgg tac	1300
Ser Trp Val Ser Leu Val	Glu Gly Tyr Leu Lys	Glu Ala Tyr Trp Tyr	
410	415	420	425
tac aat ggc tat aaa cca	agc ttg gaa gaa tat	ctc aac aac gcc aag	1348
Tyr Asn Gly Tyr Lys Pro	Ser Leu Glu Glu Tyr	Leu Asn Asn Ala Lys	
430	435	440	
att tca ata tcg gct cct	aca atc ata tcc cag	ctt tat ttt aca tta	1396
Ile Ser Ile Ser Ala Pro	Thr Ile Ile Ser Gln	Leu Tyr Phe Thr Leu	
445	450	455	
gca aac tcg att gat gaa	aca gct atc gag agc	ttg tac caa tat cat	1444
Ala Asn Ser Ile Asp Glu	Thr Ala Ile Glu Ser	Leu Tyr Gln Tyr His	
460	465	470	
aac ata ctt tac cta tca	gga acc ata tta agg	ctt gct gac gat ctt	1492
Asn Ile Leu Tyr Leu Ser	Gly Thr Ile Leu Arg	Leu Ala Asp Asp Leu	
475	480	485	
ggg aca tca caa cat gag	ctg gag aga gga gac	gta ccg aaa gca atc	1540
Gly Thr Ser Gln His Glu	Leu Glu Arg Gly Asp	Val Pro Lys Ala Ile	
490	495	500	505
cag tgc tac atg aat gac	aca aat gct tcg gag	aga gag gcg gtg gaa	1588
Gln Cys Tyr Met Asn Asp	Thr Asn Ala Ser Glu	Arg Glu Ala Val Glu	
510	515	520	
cac gtg aag ttt ctg ata	agg gag gcg tgg aag	gag atg aac acg gtc	1636
His Val Lys Phe Leu Ile	Arg Glu Ala Trp Lys	Glu Met Asn Thr Val	
525	530	535	

F08299.028E6060

aca aca gcc agc gat tgt ccg ttt acg gat gat ttg gtt gcg gcc gca 1684  
 Thr Thr Ala Ser Asp Cys Pro Phe Thr Asp Asp Leu Val Ala Ala Ala  
 540 545 550

gct aat ctt gca agg gcg gct cag ttt ata tat ctc gac ggg gat ggg 1732  
 Ala Asn Leu Ala Arg Ala Ala Gln Phe Ile Tyr Leu Asp Gly Asp Gly  
 555 560 565

cat ggc gtg caa cac tca gaa ata cat caa cag atg gga ggc ctg cta 1780  
 His Gly Val Gln His Ser Glu Ile His Gln Gln Met Gly Gly Leu Leu  
 570 575 580 585

ttc cag cct tat gtc tga ataaatcgaa aatccaacct actatgtatc 1828  
 Phe Gln Pro Tyr Val  
 590

cctcgataat atattcttgg gggttaacatg ttttaattaaa gttctaattt aaagagctga 1888  
 atcgatcctc aaaaaaaaaa aaaa 1912

<210> 54  
 <211> 590  
 <212> PRT  
 <213> *Salvia officinalis*

<400> 54  
 Met Ser Ser Ile Ser Ile Asn Ile Ala Met Pro Leu Asn Ser Leu His  
 1 5 10 15  
 Asn Phe Glu Arg Lys Pro Ser Lys Ala Trp Ser Thr Ser Cys Thr Ala  
 20 25 30  
 Pro Ala Ala Arg Leu Arg Ala Ser Ser Ser Leu Gln Gln Glu Lys Pro  
 35 40 45  
 His Gln Ile Arg Arg Ser Gly Asp Tyr Gln Pro Ser Leu Trp Asp Phe  
 50 55 60  
 Asn Tyr Ile Gln Ser Leu Asn Thr Pro Tyr Lys Glu Gln Arg His Phe  
 65 70 75 80  
 Asn Arg Gln Ala Glu Leu Ile Met Gln Val Arg Met Leu Leu Lys Val  
 85 90 95  
 Lys Met Glu Ala Ile Gln Gln Leu Glu Leu Ile Asp Asp Leu Gln Tyr  
 100 105 110  
 Leu Gly Leu Ser Tyr Phe Phe Gln Asp Glu Ile Lys Gln Ile Leu Ser  
 115 120 125  
 Ser Ile His Asn Glu Pro Arg Tyr Phe His Asn Asn Asp Leu Tyr Phe  
 130 135 140  
 Thr Ala Leu Gly Phe Arg Ile Leu Arg Gln His Gly Phe Asn Val Ser  
 145 150 155 160  
 Glu Asp Val Phe Asp Cys Phe Lys Ile Glu Lys Cys Ser Asp Phe Asn  
 165 170 175  
 Ala Asn Leu Ala Gln Asp Thr Lys Gly Met Leu Gln Leu Tyr Glu Ala  
 180 185 190  
 Ser Phe Leu Leu Arg Glu Gly Glu Asp Thr Leu Glu Leu Ala Arg Arg  
 195 200 205  
 Phe Ser Thr Arg Ser Leu Arg Glu Lys Phe Asp Glu Gly Gly Asp Glu  
 210 215 220  
 Ile Asp Glu Asp Leu Ser Ser Trp Ile Arg His Ser Leu Asp Leu Pro  
 225 230 235 240  
 Leu His Trp Arg Val Gln Gly Leu Glu Ala Arg Trp Phe Leu Asp Ala

```
<210> 55
<211> 2861
<212> DNA
<213> Abies grandis

<220>
<221> CDS
<222> (3)...(2606)
<223> abietadiene synthase
```

ag atg gcc atg cct tcc tct tca ttg tca tca cag att ccc act gct  
Met Ala Met Pro Ser Ser Ser Leu Ser Ser Gln Ile Pro Thr Ala



1				5				10				15				
gct	cat	cat	cta	act	gct	aac	gca	caa	tcc	att	ccg	cat	ttc	tcc	acg	95
Ala	His	His	Leu	Thr	Ala	Asn	Ala	Gln	Ser	Ile	Pro	His	Phe	Ser	Thr	
				20					25					30		
acg	ctg	aat	gct	gga	agc	agt	gct	agc	aaa	cgg	aga	agc	ttg	tac	cta	143
Thr	Leu	Asn	Ala	Gly	Ser	Ser	Ala	Ser	Lys	Arg	Arg	Ser	Leu	Tyr	Leu	
				35					40					45		
cga	tgg	ggt	aaa	ggt	tca	aac	aag	atc	att	gcc	tgt	gtt	gga	gaa	ggt	191
Arg	Trp	Gly	Lys	Gly	Ser	Asn	Lys	Ile	Ile	Ala	Cys	Val	Gly	Glu	Gly	
				50					55					60		
ggt	gca	acc	tct	gtt	cct	tat	cag	tct	gct	gaa	aag	aat	gat	tcg	ctt	239
Gly	Ala	Thr	Ser	Val	Pro	Tyr	Gln	Ser	Ala	Glu	Lys	Asn	Asp	Ser	Leu	
				65					70					75		
tct	tct	tct	aca	ttg	gtg	aaa	cga	gaa	ttt	cct	cca	gga	ttt	tgg	aag	287
Ser	Ser	Ser	Thr	Leu	Val	Lys	Arg	Glu	Phe	Pro	Pro	Gly	Phe	Trp	Lys	
				80					85					90		
gat	gat	ctt	atc	gat	tct	cta	acg	tca	tct	cac	aag	gtt	gca	gca	tca	335
Asp	Asp	Leu	Ile	Asp	Ser	Leu	Thr	Ser	Ser	His	Lys	Val	Ala	Ala	Ser	
				100					105					110		
gac	gag	aag	cgt	atc	gag	aca	tta	ata	tcc	gag	att	aag	aat	atg	ttt	383
Asp	Glu	Lys	Arg	Ile	Glu	Thr	Leu	Ile	Ser	Glu	Ile	Lys	Asn	Met	Phe	
				115					120					125		
aga	tgt	atg	ggc	tat	ggc	gaa	acg	aat	ccc	tct	gca	tat	gac	act	gct	431
Arg	Cys	Met	Gly	Tyr	Gly	Glu	Thr	Asn	Pro	Ser	Ala	Tyr	Asp	Thr	Ala	
				130					135					140		
tgg	gta	gca	agg	att	cca	gca	gtt	gat	ggc	tct	gac	aac	cct	cac	ttt	479
Trp	Val	Ala	Arg	Ile	Pro	Ala	Val	Asp	Gly	Ser	Asp	Asn	Pro	His	Phe	
				145					150					155		
cct	gag	acg	gtt	gaa	tgg	att	ctt	caa	aat	cag	ttg	aaa	gat	ggg	tct	527
Pro	Glu	Thr	Val	Glu	Trp	Ile	Leu	Gln	Asn	Gln	Leu	Lys	Asp	Gly	Ser	
				160					165					170		
tgg	ggt	gaa	gga	ttc	tac	ttc	ttg	gca	tat	gac	aga	ata	ctg	gct	aca	575
Trp	Gly	Glu	Gly	Phe	Tyr	Phe	Leu	Ala	Tyr	Asp	Arg	Ile	Leu	Ala	Thr	
				180					185					190		
ctt	gca	tgt	att	att	acc	ctt	acc	ctc	tgg	cgt	act	ggg	gag	aca	caa	623
Leu	Ala	Cys	Ile	Ile	Thr	Leu	Thr	Leu	Trp	Arg	Thr	Gly	Glu	Thr	Gln	
				195					200					205		
gta	cag	aaa	ggt	att	gaa	ttc	ttc	agg	aca	caa	gct	gga	aag	atg	gaa	671
Val	Gln	Lys	Gly	Ile	Glu	Phe	Phe	Arg	Thr	Gln	Ala	Gly	Lys	Met	Glu	
				210					215					220		
gat	gaa	gct	gat	agt	cat	agg	cca	agt	gga	ttt	gaa	ata	gta	ttt	cct	719
Asp	Glu	Ala	Asp	Ser	His	Arg	Pro	Ser	Gly							

gca atg cta aag gaa gct aaa atc tta ggc ttg gat ctg cct tac gat	767
Ala Met Leu Lys Glu Ala Lys Ile Leu Gly Leu Asp Leu Pro Tyr Asp	
240 245 250 255	
ttg cca ttc ctg aaa caa atc atc gaa aag cgg gag gct aag ctt aaa	815
Leu Pro Phe Leu Lys Gln Ile Ile Glu Lys Arg Glu Ala Lys Leu Lys	
260 265 270	
agg att ccc act gat gtt ctc tat gcc ctt cca aca acg tta ttg tat	863
Arg Ile Pro Thr Asp Val Leu Tyr Ala Leu Pro Thr Thr Leu Leu Tyr	
275 280 285	
tct ttg gaa ggt tta caa gaa ata gta gac tgg cag aaa ata atg aaa	911
Ser Leu Glu Gly Leu Gln Glu Ile Val Asp Trp Gln Lys Ile Met Lys	
290 295 300	
ctt caa tcc aag gat gga tca ttt ctc agc tct ccg gca tct aca gcg	959
Leu Gln Ser Lys Asp Gly Ser Phe Leu Ser Ser Pro Ala Ser Thr Ala	
305 310 315	
gct gta ttc atg cgt aca ggg aac aaa aag tgc ttg gat ttc ttg aac	1007
Ala Val Phe Met Arg Thr Gly Asn Lys Lys Cys Leu Asp Phe Leu Asn	
320 325 330 335	
ttt gtc ttg aag aaa ttc gga aac cat gtg cct tgt cac tat ccg ctt	1055
Phe Val Leu Lys Lys Phe Gly Asn His Val Pro Cys His Tyr Pro Leu	
340 345 350	
gat cta ttt gaa cgt ttg tgg gcg gtt gat aca gtt gag cgg cta ggt	1103
Asp Leu Phe Glu Arg Leu Trp Ala Val Asp Thr Val Glu Arg Leu Gly	
355 360 365	
atc gat cgt cat ttc aaa gag gag atc aag gaa gca ttg gat tat gtt	1151
Ile Asp Arg His Phe Lys Glu Glu Ile Lys Glu Ala Leu Asp Tyr Val	
370 375 380	
tac agc cat tgg gac gaa aga ggc att gga tgg gcg aga gag aat cct	1199
Tyr Ser His Trp Asp Glu Arg Gly Ile Gly Trp Ala Arg Glu Asn Pro	
385 390 395	
gtt cct gat att gat gat aca gcc atg ggc ctt cga atc ttg aga tta	1247
Val Pro Asp Ile Asp Thr Ala Met Gly Leu Arg Ile Leu Arg Leu	
400 405 410 415	
cat gga tac aat gta tcc tca gat gtt tta aaa aca ttt aga gat gag	1295
His Gly Tyr Asn Val Ser Ser Asp Val Leu Lys Thr Phe Arg Asp Glu	
420 425 430	
aat ggg gag ttc ttt tgc ttc ttg ggt caa aca cag aga gga gtt aca	1343
Asn Gly Glu Phe Phe Cys Phe Leu Gly Gln Thr Gln Arg Gly Val Thr	
435 440 445	
gac atg tta aac gtc aat cgt tgt tca cat gtt tca ttt ccg gga gaa	1391
Asp Met Leu Asn Val Asn Arg Cys Ser His Val Ser Phe Pro Gly Glu	
450 455 460	

acg Thr	atc Ile	atg Met	gaa Glu	gaa Glu	gca Ala	aaa Lys	ctc Leu	tgt Cys	acc Thr	gaa Glu	agg Arg	tat Tyr	ctg Leu	agg Arg	aat Asn	1439
465			470			475										
gct Ala	ctg Leu	gaa Glu	aat Asn	gtg Val	gat Asp	gcc Ala	ttt Phe	gac Asp	aaa Lys	tgg Trp	gct Ala	ttt Phe	aaa Lys	aag Lys	aat Asn	1487
480			485			490			495							
att Ile	cgg Arg	gga Gly	gag Glu	gta Val	gag Glu	tat Tyr	gca Ala	ctc Leu	aaa Lys	tat Tyr	ccc Pro	tgg Trp	cat His	aag Lys	agt Ser	1535
500			505			510										
atg Met	cca Pro	agg Arg	ttg Leu	gag Glu	gct Ala	aga Arg	agc Ser	tat Tyr	att Ile	gaa Glu	aac Asn	tat Tyr	ggg Gly	cca Pro	gat Asp	1583
515			520			525										
gat Asp	gtg Val	tgg Trp	ctt Leu	gga Gly	aaa Lys	act Thr	gta Val	tat Tyr	atg Met	atg Met	cca Pro	tac Tyr	att Ile	tcg Ser	aat Asn	1631
530			535			540										
gaa Glu	aag Lys	tat Tyr	tta Leu	gaa Glu	cta Leu	gcg Ala	aaa Lys	ctg Leu	gac Asp	ttc Phe	aat Asn	aag Lys	gtg Val	cag Gln	tct Ser	1679
545			550			555										
ata Ile	cac His	caa Gln	aca Thr	gag Glu	ctt Leu	caa Gln	gat Asp	ctt Leu	cga Arg	agg Arg	tgg Trp	tgg Trp	aaa Lys	tca Ser	tcc Ser	1727
560			565			570										
ggt Gly	ttc Phe	acg Thr	gat Asp	ctg Leu	aat Asn	ttc Phe	act Thr	cgt Arg	gag Glu	cgt Arg	gtg Val	acg Thr	gaa Glu	ata Ile	tat Tyr	1775
580			585			590										
ttc Phe	tca Ser	ccg Pro	gca Ala	tcc Ser	ttt Phe	atc Ile	ttt Phe	gag Glu	ccc Pro	gag Glu	ttt Phe	tct Ser	aag Lys	tgc Cys	aga Arg	1823
595			600			605										
gag Glu	gtt Val	tat Tyr	aca Thr	aaa Lys	act Thr	tcc Ser	aat Asn	ttc Phe	act Thr	gtt Val	att Ile	tta Leu	gat Asp	gat Asp	ctt Leu	1871
610			615			620										
tat Tyr	gac Asp	gcc Ala	cat His	gga Gly	tct Ser	tta Leu	gac Asp	gat Asp	ctt Leu	aag Lys	ttg Leu	ttc Phe	aca Thr	gaa Glu	tca Ser	1919
625			630			635										
gtc Val	aaa Lys	aga Arg	tgg Trp	gat Asp	cta Leu	tca Ser	cta Leu	gtg Val	gac Asp	caa Gln	atg Met	cca Pro	caa Gln	caa Gln	atg Met	1967
640			645			650			655							
aaa Lys	ata Ile	tgt Cys	ttt Phe	gtg Val	ggt Gly	ttc Phe	tac Tyr	aat Asn	act Thr	ttt Phe	aat Asn	gat Asp	ata Ile	gca Ala	aaa Lys	2015
660			665			670										
gaa Glu	gga Gly	cgt Arg	gag Glu	agg Arg	caa Gln	ggg Gly	cgc Arg	gat Asp	gtg Val	cta Leu	ggc Gly	tac Tyr	att Ile	caa Gln	aat Asn	2063
675			680			685										
gtt Glu	tgg Glu	aaa Glu	gtc Glu	caa Glu	ctt Glu	gaa Glu	gct Glu	tac Glu	acg Glu	aaa Glu	gaa Glu	gca Glu	gaa Glu	tgg Glu	tct Glu	2111

```
<210> 56
<211> 868
<212> PRT
<213> Abies grandis
```

&lt;400&gt; 56

Met	Ala	Met	Pro	Ser	Ser	Ser	Leu	Ser	Ser	Gln	Ile	Pro	Thr	Ala	Ala
1				5					10					15	
His	His	Leu	Thr	Ala	Asn	Ala	Gln	Ser	Ile	Pro	His	Phe	Ser	Thr	Thr
		20						25					30		
Leu	Asn	Ala	Gly	Ser	Ser	Ala	Ser	Lys	Arg	Arg	Ser	Leu	Tyr	Leu	Arg
	35						40					45			
Trp	Gly	Lys	Gly	Ser	Asn	Lys	Ile	Ile	Ala	Cys	Val	Gly	Glu	Gly	Gly
	50					55					60				
Ala	Thr	Ser	Val	Pro	Tyr	Gln	Ser	Ala	Glu	Lys	Asn	Asp	Ser	Leu	Ser
65					70					75					80
Ser	Ser	Thr	Leu	Val	Lys	Arg	Glu	Phe	Pro	Pro	Gly	Phe	Trp	Lys	Asp
				85					90					95	
Asp	Leu	Ile	Asp	Ser	Leu	Thr	Ser	Ser	His	Lys	Val	Ala	Ala	Ser	Asp
			100					105					110		
Glu	Lys	Arg	Ile	Glu	Thr	Leu	Ile	Ser	Glu	Ile	Lys	Asn	Met	Phe	Arg
	115						120					125			
Cys	Met	Gly	Tyr	Gly	Glu	Thr	Asn	Pro	Ser	Ala	Tyr	Asp	Thr	Ala	Trp
	130					135						140			
Val	Ala	Arg	Ile	Pro	Ala	Val	Asp	Gly	Ser	Asp	Asn	Pro	His	Phe	Pro
145					150					155					160
Glu	Thr	Val	Glu	Trp	Ile	Leu	Gln	Asn	Gln	Leu	Lys	Asp	Gly	Ser	Trp
			165						170					175	
Gly	Glu	Gly	Phe	Tyr	Phe	Leu	Ala	Tyr	Asp	Arg	Ile	Leu	Ala	Thr	Leu
			180					185					190		
Ala	Cys	Ile	Ile	Thr	Leu	Thr	Leu	Trp	Arg	Thr	Gly	Glu	Thr	Gln	Val
	195						200					205			
Gln	Lys	Gly	Ile	Glu	Phe	Phe	Arg	Thr	Gln	Ala	Gly	Lys	Met	Glu	Asp
	210					215					220				
Glu	Ala	Asp	Ser	His	Arg	Pro	Ser	Gly	Phe	Glu	Ile	Val	Phe	Pro	Ala
225					230					235					240
Met	Leu	Lys	Glu	Ala	Lys	Ile	Leu	Gly	Leu	Asp	Leu	Pro	Tyr	Asp	Leu
			245					250						255	
Pro	Phe	Leu	Lys	Gln	Ile	Ile	Glu	Lys	Arg	Glu	Ala	Lys	Leu	Lys	Arg
			260					265						270	
Ile	Pro	Thr	Asp	Val	Leu	Tyr	Ala	Leu	Pro	Thr	Thr	Leu	Leu	Tyr	Ser
		275					280						285		
Leu	Glu	Gly	Leu	Gln	Glu	Ile	Val	Asp	Trp	Gln	Lys	Ile	Met	Lys	Leu
290					295						300				
Gln	Ser	Lys	Asp	Gly	Ser	Phe	Leu	Ser	Ser	Pro	Ala	Ser	Thr	Ala	Ala
305					310					315					320
Val	Phe	Met	Arg	Thr	Gly	Asn	Lys	Lys	Cys	Leu	Asp	Phe	Leu	Asn	Phe
			325						330					335	
Val	Leu	Lys	Lys	Phe	Gly	Asn	His	Val	Pro	Cys	His	Tyr	Pro	Leu	Asp
			340					345						350	
Leu	Phe	Glu	Arg	Leu	Trp	Ala	Val	Asp	Thr	Val	Glu	Arg	Leu	Gly	Ile
		355					360					365			
Asp	Arg	His	Phe	Lys	Glu	Glu	Ile	Lys	Glu	Ala	Leu	Asp	Tyr	Val	Tyr
	370					375					380				
Ser	His	Trp	Asp	Glu	Arg	Gly	Ile	Gly	Trp	Ala	Arg	Glu	Asn	Pro	Val
385					390					395					400
Pro	Asp	Ile	Asp	Asp	Thr	Ala	Met	Gly	Leu	Arg	Ile	Leu	Arg	Leu	His
			405						410					415	
Gly	Tyr	Asn	Val	Ser	Ser	Asp	Val	Leu	Lys	Thr	Phe	Arg	Asp	Glu	Asn
			420					425					430		
Gly	Glu	Phe	Cys	Phe	Leu	Gly	Gln	Thr	Gln	Arg	Gly	Val	Thr	Asp	
	435					440					445				

PDB: 1D30" 02222222

<210>	57
<211>	2089

tct act ttt cct gat ctc aac tcg act gcc ttg gcg ctt cga act ctt 639  
Ser Thr Phe Pro Asp Leu Asn Ser Thr Ala Leu Ala Leu Arg Thr Leu  
175 180 185

cga Arg 190	ctg Leu	cac His	gga Gly	tac Tyr	aat Asn 195	gtg Val	tct Ser	tca Ser	gat Asp	gtg Val 200	ctg Leu	gaa Glu	tac Tyr	ttc Phe	aaa Lys 205	687
gat Asp	gaa Glu	aag Lys	ggg Gly	cat His 210	ttt Phe	gcc Ala	tgc Cys	cct Pro	gca Ala 215	atc Ile	cta Leu	acc Thr	gag Glu	gga Gly 220	cag Gln	735
atc Ile	act Thr	aga Arg	agt Ser 225	gtt Val	cta Leu	aat Asn	tta Leu	tat Tyr 230	cgg Arg	gct Ala	tcc Ser	ctg Leu	gtc Val 235	gcc Ala	ttt Phe	783
ccc Pro	ggg Gly	gag Glu 240	aaa Lys	gtt Val	atg Met	gaa Glu	gag Glu 245	gct Ala	gaa Glu	atc Ile	ttc Phe	tcg Ser 250	gca Ala	tct Ser	tat Tyr	831
ttg Leu	aaa Lys 255	aaa Lys	gtc Val	tta Leu	caa Gln 260	aag Lys	att Ile	ccg Pro	gtc Val	tcc Ser 265	aat Asn	ctt Leu	tca Ser	gga Gly	gag Glu	879
ata Ile 270	gaa Glu	tat Tyr	gtt Val	ttg Leu	gaa Glu 275	tat Tyr	ggg Gly	tgg Trp	cac His	acg Thr 280	aat Asn	ttg Leu	ccg Pro	aga Arg	ttg Leu 285	927
gaa Glu	gca Ala	aga Arg	aat Asn 290	tat Tyr	atc Ile	gag Glu	gtc Val	tac Tyr 295	gag Glu	cag Gln	agc Ser	ggc Gly	tat Tyr 300	gaa Glu	agc Ser	975
tta Leu	aac Asn	gag Glu	atg Met 305	cca Pro	tat Tyr	atg Met	aac Asn	atg Met 310	aag Lys	aag Lys	ctt Leu	tta Leu	caa Gln 315	ctt Leu	gca Ala	1023
aaa Lys	ttg Leu	gag Glu 320	ttc Phe	aat Asn	atc Ile	ttt Phe 325	cac His	tct Ser	ttg Leu	caa Gln	cta Leu 330	aga Arg	gag Glu	tta Leu	caa Gln	1071
tct Ser	atc Ile 335	tcc Ser	aga Arg	tgg Trp	tgg Trp	aaa Lys 340	gaa Glu	tca Ser	ggg Gly	tcc Ser 345	tct Ser	caa Gln	ctg Leu	act Thr	ttt Phe	1119
aca Thr 350	cgg Arg	cat His	cgt Arg	cac His	gtg Val 355	gaa Glu	tac Tyr	tac Tyr	act Thr	atg Met 360	gca Ala	tct Ser	tgc Cys	att Ile	tct Ser 365	1167
atg Met	ttg Leu	cca Pro	aaa Lys	cat His 370	tca Ser	gct Ala	ttc Phe	aga Arg	atg Met 375	gag Glu	ttt Phe	gtc Val	aaa Lys	gtg Val 380	tgt Cys	1215
cat His	ctt Leu	gta Val	aca Thr 385	gtt Val	ctc Leu	gat Asp	gat Asp	ata Ile 390	tat Tyr	gac Asp	act Thr	ttt Phe	gga Gly 395	aca Thr	atg Met	1263
aac Asn	gaa Glu	ctc Leu 400	caa Gln	ctt Leu	ttt Phe	acg Thr	gat Asp 405	gca Ala	att Ile	aag Lys	aga Arg	tgg Trp 410	gat Asp	ttg Leu	tca Ser	1311



acg	aca	agg	tgg	ctt	cca	gaa	tat	atg	aaa	gga	gtg	tac	atg	gac	ttg	1359
Thr	Thr	Arg	Trp	Leu	Pro	Glu	Tyr	Met	Lys	Gly	Val	Tyr	Met	Asp	Leu	
	415					420					425					
tat	caa	tgc	att	aat	gaa	atg	gtg	gaa	gag	gct	gag	aag	act	caa	ggc	1407
Tyr	Gln	Cys	Ile	Asn	Glu	Met	Val	Glu	Glu	Ala	Glu	Lys	Thr	Gln	Gly	
430					435					440					445	
cga	gat	atg	ctc	aac	tat	att	caa	aat	gct	tgg	gaa	gcc	cta	ttt	gat	1455
Arg	Asp	Met	Leu	Asn	Tyr	Ile	Gln	Asn	Ala	Trp	Glu	Ala	Leu	Phe	Asp	
				450					455					460		
acc	ttt	atg	caa	gaa	gca	aag	tgg	atc	tcc	agc	agt	tat	ctc	cca	acg	1503
Thr	Phe	Met	Gln	Glu	Ala	Lys	Trp	Ile	Ser	Ser	Ser	Tyr	Leu	Pro	Thr	
			465					470					475			
ttt	gag	gag	tac	ttg	aag	aat	gca	aaa	gtt	agt	tct	ggt	tct	cgc	ata	1551
Phe	Glu	Glu	Tyr	Leu	Lys	Asn	Ala	Lys	Val	Ser	Ser	Gly	Ser	Arg	Ile	
		480					485					490				
gcc	aca	tta	caa	ccc	att	ctc	act	ttg	gat	gta	cca	ctt	cct	gat	tac	1599
Ala	Thr	Leu	Gln	Pro	Ile	Leu	Thr	Leu	Asp	Val	Pro	Leu	Pro	Asp	Tyr	
	495					500					505					
ata	ctg	caa	gaa	att	gat	tat	cca	tcc	aga	ttc	aat	gag	tta	gct	tcg	1647
Ile	Leu	Gln	Glu	Ile	Asp	Tyr	Pro	Ser	Arg	Phe	Asn	Glu	Leu	Ala	Ser	
510					515					520					525	
tcc	atc	ctt	cga	cta	cga	ggt	gac	acg	cgc	tgc	tac	aag	gcg	gat	agg	1695
Ser	Ile	Leu	Arg	Leu	Arg	Gly	Asp	Thr	Arg	Cys	Tyr	Lys	Ala	Asp	Arg	
				530					535					540		
gcc	cgt	gga	gaa	gaa	gct	tca	gct	ata	tcg	tgt	tat	atg	aaa	gac	cat	1743
Ala	Arg	Gly	Glu	Glu	Ala	Ser	Ala	Ile	Ser	Cys	Tyr	Met	Lys	Asp	His	
			545					550					555			
cct	gga	tca	ata	gag	gaa	gat	gct	ctc	aat	cat	atc	aac	gcc	atg	atc	1791
Pro	Gly	Ser	Ile	Glu	Glu	Asp	Ala	Leu	Asn	His	Ile	Asn	Ala	Met	Ile	
		560					565					570				
agt	gat	gca	atc	aga	gaa	tta	aat	tgg	gag	ctt	ctc	aga	ccg	gat	agc	1839
Ser	Asp	Ala	Ile	Arg	Glu	Leu	Asn	Trp	Glu	Leu	Leu	Arg	Pro	Asp	Ser	
	575					580					585					
aaa	agt	ccc	atc	tct	tcc	aag	aaa	cat	gct	ttt	gac	atc	acc	aga	gct	1887
Lys	Ser	Pro	Ile	Ser	Ser	Lys	Lys	His	Ala	Phe	Asp	Ile	Thr	Arg	Ala	
590					595					600					605	
ttc	cat	cat	gtc	tac	aaa	tat	cga	gat	ggt	tac	act	gtt	tcc	aac	aac	1935
Phe	His	His	Val	Tyr	Lys	Tyr	Arg	Asp	Gly	Tyr	Thr	Val	Ser	Asn	Asn	
			610						615					620		
gaa	aca	aag	aat	ttg	gtg	atg	aaa	acc	gtt	ctt						

2089

<211> 637

<212> PRT

<213> Abies grandis

<400> 58

Met 1	Ala	Leu	Leu	Ser 5	Ile	Val	Ser	Leu	Gln	Val	Pro	Lys	Ser	Cys 15	Gly
Leu	Lys	Ser	Leu	Ile	Ser	Ser	Ser	Asn	Val	Gln	Lys	Ala	Leu	Cys 30	Ile
Ser	Thr	Ala	Val	Pro	Thr	Leu	Arg	Met	Arg	Arg	Arg	Gln	Lys	Ala	Leu
Val	Ile	Asn	Met	Lys	Leu	Thr	Thr	Val	Ser	His	Arg	Asp	Asp	Asn	Gly
Gly 65	Gly	Val	Leu	Gln	Arg	Arg	Ile	Ala	Asp	His	His	Pro	Asn	Leu	Trp 80
Glu	Asp	Asp	Phe	Ile	Gln	Ser	Leu	Ser	Ser	Pro	Tyr	Gly	Gly	Ser	Ser
Tyr	Ser	Glu	Arg	Ala	Glu	Thr	Val	Val	Glu	Glu	Val	Lys	Glu	Met	Phe
Asn	Ser	Ile	Pro	Asn	Asn	Arg	Glu	Leu	Phe	Gly	Ser	Gln	Asn	Asp	Leu
Leu	Thr	Arg	Leu	Trp	Met	Val	Asp	Ser	Ile	Glu	Arg	Leu	Gly	Ile	Asp
Arg 145	His	Phe	Gln	Asn	Glu	Ile	Arg	Val	Ala	Leu	Asp	Tyr	Val	Tyr	Ser
Tyr	Trp	Lys	Glu	Lys	Glu	Gly	Ile	Gly	Cys	Gly	Arg	Asp	Ser	Thr	Phe
Pro	Asp	Leu	Asn	Ser	Thr	Ala	Leu	Ala	Leu	Arg	Thr	Leu	Arg	Leu	His
Gly	Tyr	Asn	Val	Ser	Ser	Asp	Val	Leu	Glu	Tyr	Phe	Lys	Asp	Glu	Lys
Gly	His	Phe	Ala	Cys	Pro	Ala	Ile	Leu	Thr	Glu	Gly	Gln	Ile	Thr	Arg
Ser 225	Val	Leu	Asn	Leu	Tyr	Arg	Ala	Ser	Leu	Val	Ala	Phe	Pro	Gly	Glu
Lys	Val	Met	Glu	Glu	Ala	Glu	Ile	Phe	Ser	Ala	Ser	Tyr	Leu	Lys	Lys
Val	Leu	Gln	Lys	Ile	Pro	Val	Ser	Asn	Leu	Ser	Gly	Glu	Ile	Glu	Tyr
Val	Leu	Glu	Tyr	Gly	Trp	His	Thr	Asn	Leu	Pro	Arg	Leu	Glu	Ala	Arg
Asn	Tyr	Ile	Glu	Val	Tyr	Glu	Gln	Ser	Gly	Tyr	Glu	Ser	Leu	Asn	Glu
Met 305	Pro	Tyr	Met	Asn	Met	Lys	Lys	Leu	Leu	Gln	Leu	Ala	Lys	Leu	Glu
Phe	Asn	Ile	Phe	His	Ser	Leu	Gln	Leu	Arg	Glu	Leu	Gln	Ser	Ile	Ser
Arg	Trp	Trp	Lys	Glu	Ser	Gly	Ser	Ser	Gln	Leu	Thr	Phe	Thr	Arg	His
Arg	His	Val	Glu	Tyr	Tyr	Thr	Met	Ala	Ser	Cys	Ile	Ser	Met	Leu	Pro
Lys	His	Ser	Ala	Phe	Arg	Met	Glu	Phe	Val	Lys	Val	Cys	His	Leu	Val
Thr	Val	Leu	Asp	Asp	Ile	Tyr	Asp	Thr	Phe	Gly	Thr	Met	Asn	Glu	Leu

385					390					395					400
Gln	Leu	Phe	Thr	Asp	Ala	Ile	Lys	Arg	Trp	Asp	Leu	Ser	Thr	Thr	Arg
				405					410					415	
Trp	Leu	Pro	Glu	Tyr	Met	Lys	Gly	Val	Tyr	Met	Asp	Leu	Tyr	Gln	Cys
			420					425					430		
Ile	Asn	Glu	Met	Val	Glu	Glu	Ala	Glu	Lys	Thr	Gln	Gly	Arg	Asp	Met
		435					440					445			
Leu	Asn	Tyr	Ile	Gln	Asn	Ala	Trp	Glu	Ala	Leu	Phe	Asp	Thr	Phe	Met
	450					455					460				
Gln	Glu	Ala	Lys	Trp	Ile	Ser	Ser	Ser	Tyr	Leu	Pro	Thr	Phe	Glu	Glu
465					470				475					480	
Tyr	Leu	Lys	Asn	Ala	Lys	Val	Ser	Ser	Gly	Ser	Arg	Ile	Ala	Thr	Leu
			485						490					495	
Gln	Pro	Ile	Leu	Thr	Leu	Asp	Val	Pro	Leu	Pro	Asp	Tyr	Ile	Leu	Gln
			500					505					510		
Glu	Ile	Asp	Tyr	Pro	Ser	Arg	Phe	Asn	Glu	Leu	Ala	Ser	Ser	Ile	Leu
		515					520					525			
Arg	Leu	Arg	Gly	Asp	Thr	Arg	Cys	Tyr	Lys	Ala	Asp	Arg	Ala	Arg	Gly
	530					535					540				
Glu	Glu	Ala	Ser	Ala	Ile	Ser	Cys	Tyr	Met	Lys	Asp	His	Pro	Gly	Ser
545					550					555				560	
Ile	Glu	Glu	Asp	Ala	Leu	Asn	His	Ile	Asn	Ala	Met	Ile	Ser	Asp	Ala
			565						570					575	
Ile	Arg	Glu	Leu	Asn	Trp	Glu	Leu	Leu	Arg	Pro	Asp	Ser	Lys	Ser	Pro
			580					585					590		
Ile	Ser	Ser	Lys	Lys	His	Ala	Phe	Asp	Ile	Thr	Arg	Ala	Phe	His	His
		595				600						605			
Val	Tyr	Lys	Tyr	Arg	Asp	Gly	Tyr	Thr	Val	Ser	Asn	Asn	Glu	Thr	Lys
	610					615					620				
Asn	Leu	Val	Met	Lys	Thr	Val	Leu	Glu	Pro	Leu	Ala	Leu			
625					630					635					

108230-000000